

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: July 15, 2002, 06:40:44 ; Search time 1825.85 Seconds  
(without alignments)  
14750.638 Million cell updates/sec

Title: US-09-889-926-1

Perfect score: 1287  
Sequence: 1 gtcgaccacgctcgtctt.....aaaaaaaaagggcgccgc 1287

Scoring table: IDENTITY.NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.\*

1: gb\_ba.\*

2: gb\_hgt.\*

3: gb\_in.\*

4: gb\_om.\*

5: gb\_ov.\*

6: gb\_pat.\*

7: gb\_ph.\*

8: gb\_pl.\*

9: gb\_pr.\*

10: gb\_ro.\*

11: gb\_sts.\*

12: gb\_sy.\*

13: gb\_un.\*

14: gb\_vi.\*

15: em\_ba.\*

16: em\_fun.\*

17: em\_hum.\*

18: em\_in.\*

19: em\_mu.\*

20: em\_om.\*

21: em\_or.\*

22: em\_ov.\*

23: em\_pat.\*

24: em\_ph.\*

25: em\_pl.\*

26: em\_ro.\*

27: em\_sts.\*

28: em\_un.\*

29: em\_vi.\*

30: em\_htg\_hum.\*

31: em\_htg\_inv.\*

32: em\_htg\_other.\*

33: em\_htgo\_inv.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
-----					

1	1272	98.8	1272	8	AF198054	Arabidops
2	856.4	66.5	96489	8	AC009894	Arabidops
3	856.4	66.5	106320	8	AC002304	Genomic s
4	278.6	21.6	1206	8	AF402602	Phaseolus
5	176.6	13.7	1188	8	AY056327	Arabidops
6	167.2	13.0	81020	8	AB026845	Arabidops
7	162	12.6	1277	8	AB026845	Arabidops
8	157	12.2	1471	8	AY054644	Arabidops
9	156.2	12.1	1307	8	AF361623	Arabidops
10	144.6	11.2	1173	8	AY062638	Arabidops
11	143.4	11.1	1100	8	PHRNANAM	X92205 P hybrid m
12	143	11.1	147640	2	AF402603	Phaseolus
13	143	11.1	157274	2	AP003542	Arabidops
14	142	11.0	538	8	AP004679	Arabidops
15	142	11.0	1109	8	AY051015	Arabidops
16	137.4	10.7	961	8	AF360201	Arabidops
17	135.2	10.5	1230	8	AB049069	Arabidops
18	135.2	10.5	1701	8	AF428375	Arabidops
19	134.6	10.5	1202	8	AY057578	Arabidops
20	130.4	10.1	1226	8	AY045843	Arabidops
21	128.2	10.0	138936	2	AY065268	Arabidops
22	125.2	9.7	1216	8	AP004563	Arabidops
23	125	9.7	954	8	ATAATAF2	X74756 A thaliana
24	124.4	9.7	68697	8	AB049070	Arabidops
25	122.6	9.5	50156	8	AB012243	Arabidops
26	121.6	9.4	1295	8	AC005310	Arabidops
27	120	9.3	1264	8	STU401151	Arabidops
28	120	9.3	80376	8	AB010073	Oryza sat
29	119.6	9.3	88989	8	AB028183	Arabidops
30	116.8	9.1	81736	8	AB019235	Arabidops
31	115.8	9.0	1090	6	AB026658	Arabidops
32	115.8	9.0	1090	8	AB2384	Arabidops
33	115.4	9.0	94695	8	TSP010829	Arabidops
34	115.4	9.0	195452	8	ATF23E13	Arabidops
35	115	8.9	18212	8	ATCHRIV84	Arabidops
36	114.2	8.9	80413	8	AP000388	Arabidops
37	113.8	8.8	1423	8	AC021665	Arabidops
38	113.4	8.8	63654	8	AB028185	Arabidops
39	113.4	8.8	110804	8	ATAC011698	Arabidops
40	113.2	8.8	174264	2	ATAC016829	Arabidops
41	113	8.8	81609	8	OSJN00003	Arabidops
42	113	8.8	94487	8	AC027035	Oryza sat
43	113	8.8	100806	8	AC012394	Arabidops
44	112.4	8.7	780	8	AC015450	Arabidops
45	112	8.7	2427	8	AY061835	Streptoca
					ART222713	Arabidops

#### ALIGNMENTS

RESULT 1

AF198054

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

AF198054

Arabidopsis thaliana

1272 bp mRNA linear

PLN 13-DEC-2000

complete cds.

GI:6649235

thale cress.

Arabidopsis thaliana

Eukaryota; Viridiplantae;

Streptophyta; Tracheophyta;

Spermatophyta; Magnoliophyta;

eudicotyledons; core eudicots;

Rosidae; eurosids II; Brassicales;

Brassicaceae; Arabidopsis.

1 (bases 1 to 1272)

Xie,Q., Frugis,G., Colgan,D. and Chua,N.H.

Arabidopsis NAC1 transduces auxin signal downstream of TIR1 to

promote lateral root development

Genes Dev. 14 (23), 3024-3036 (2000)

20566646

2 (bases 1 to 1272)

Xie,Q. and Chua,N.H.

Direct Submission

Submitted (24-OCT-1999) plant Cell Biology, Institute of Molecular

Agrobiology, 1 Research Link, The National University of Singapore

601	GAATACGGAAGAGGTATATCTAGAGACAACATGGGAAGCTGTGTTTGTATGACAGACAGCCTC	660
661	tgatcgcttctccactgatgatccttacaatcaacttgcgaagacccctcttcttta	720
661	TGCATCGCTTCTCCATGATGGATCCTTACATCAACTTTGACCAAGAACCCCTCTCTTA	720
721	tctcagtgatgatcactacatcatcaatgaagcagctacccctgcttctccaattgtc	780
721	TCTCAGTGATGATCATTACTACATCATCAATGAGCAGGTACCTGCTTCTCCAATTTGTC	780
781	acagaacccaaaccttaactcgaaaccttaacccactcagctcgtctgaactcaagattccatg	840
781	ACAGAACCAAAACCTTAAACTCGAACCTTAAGCAACTCAGTCTCTGAACTCAAGATTCCATG	840
841	caagaacccaaaccttgaactgtgtgttcagctcagccacgacgctcacaggtcctga	900
841	CAAGAACCCTAACCCCTTTTACTTGGTGTTCAGCTCAGCCACGCTCAGAGGCTCGA	900
901	ctcattctgttctcagatcagatggttctcagagctcactcagtcagctcactaagat	960
901	CTCATTTCTTCTCAGATCAGATGGTTCTCAGAGCTCTACTCAGTCAGTCCTCAAGAT	960
961	tgatggaagctcgggacctaaagaatcacagagttatggagaagtagctcgaagagcct	1020
961	TGATGGAAGCCCTCGGGCCTAAGAAATCACAGAGTATGGAGAAGTAGTTCGGAGAGCCT	1020
1021	cctgaccgacatcggtattccaaagcaactgtttggaattgctgatgcagtgtaacgag	1080
1021	CCTGACCGACATCGGTATTTCCAAGCAGCTGTTTGGAAATTTGCTGATGATCGAGTGAACGAG	1080
1081	agttactatgctatatctctatccatgattggagaacattcttcggggggaataacgtg	1140
1081	AGTTACTATTGCTATTATTCCTATCCATGATTTGGAACAATTTCTCGGGGGGAAATACGGT	1140
1141	tgctgtcgtatgtacaaaactttccctcactcttaccacaggtagatcctcgtataaa	1200
1141	TGCTTGTCTGATGTGACAAACATTTCCCTCACTCTGTACCCACAGTAGATTCAATGTA	1200
1201	taccacttatgcgctagacatcacatatattcctcagtagtccattgtttccaaaaaa	1260
1201	TAGCACTTATGACGCTAGACATACATATATTTCATCTAGTTCATTGTTTCAAAAAA	1260
1261	aaaaaaaaaaaa 1272	
1261	AAAAAAAAAAAAA 1272	
RESULT	2	
AC009894	96489 bp	linear
LOCUS	66489 bp	PLN 07-DEC-1999
DEFINITION	Arabidopsis thaliana chromosome I BAC T6H22 genomic sequence,	
ACCESSION	complete sequence.	
VERSION	AC009894	
KEYWORDS	AC009894.2	GI:5902358
SOURCE	HTG.	
ORGANISM	thale cress.	
REFERENCE	Arabidopsis thaliana	
AUTHORS	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis. 1 (bases 1 to 96489)	
JOURNAL	Federspiel, N.A., Palm, C.J., Conway, A.B., Conn, L., Hansen, N.F., Alfafi, H., Nguyen, M., Lam, B., Buehler, E., Dunn, P., Gonzalez, A., Kremenetskaia, I., Kim, C., Lenz, C., Li, J., Liu, S., Luros, S., Schwartz, J., Shinn, P., Toriumi, M., Vyotskaia, V., Walker, M., Yu, G., Ecker, J., Theologis, A. and Davis, R.W.	
REFERENCE	Unpublished	
AUTHORS	2 (bases 1 to 96489)	

TITLE JOURNAL	Direct Submission Submitted (04-SEP-1999) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA	gene	NDAFGTAHRAHASTEGVTKFLKPSVAGFLLOKELDYLGVAVSNPKRPFAAIVGGSKVS SKIGVIESLLEKCDILLGGGMIFTFYKRAQGLSVSSSLEEEDKL"
REFERENCE AUTHORS	3 (bases 1 to 96489) Federspiel, N.A., Palm, C.J., Conway, A.B., Conn, L., Hansen, N.F., Altafi, H., Nguyen, M., Lam, B., Buehler, E., Dunn, P., Gonzalez, A., Kremenetskaia, I., Kim, C., Lenz, C., Li, J., Liu, S., Luross, S., Schwartz, J., Shinn, P., Toriumi, M., Vyotskaia, V., Walker, M., Yu, G., Ecker, J., Theologis, A. and Davis, R.W.	CDS	/gene="T6H22.2" Join(1728..2082,3382..2690,2774..2850,2968..3044, 3126..3258,3377..3532) /note="Hypothetical protein" /codon_start=1 /protein_id="AAF02831.1" /db_xref="GI:6056367"
TITLE JOURNAL	Direct Submission Submitted (16-SEP-1999) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA	gene	/translation="MALSPSPCLRSLSPSRQIGFLVPRVQSLVFGSVRKHELRR PSALREYEDAVKRLDLAGALRKLKSEIENDEQDSVESIVTAKLSGLGALELERDW QVLDACLNADDMRLVGIIFDXSGDGLNFCYCLVWLTCLSPKKGWLGSSGIALAAL LGVSYLLSODEIDVRNLAVILGLVLDVFLGCLAQVSCYMPHPKRRIVVHEAGH LLVAYLMCCPIRGVILDPVAMQGVQAGTQFDWDKMESEIAGRLSGSSFPDRYSM VIFAGTAAAEALQVGSPLSIVIRIEEAMSSK" /complement(4058..4471) /gene="T6H22.3" /note="hap5b" /complement(4058..4471) /gene="T6H22.3"
REFERENCE AUTHORS	4 (bases 1 to 96489) Federspiel, N.A., Palm, C.J., Conway, A.B., Conn, L., Hansen, N.F., Altafi, H., Araujo, R., Huizar, L., Rowley, D., Brooks, S., Buehler, E., Chao, Q., Dunn, P., Gonzalez, A., Khan, S., Kremenetskaia, I., Kim, C., Lenz, C., Li, J., Liu, S., Luross, S., Schwartz, J., Shinn, P., Toriumi, M., Vyotskaia, V., Yu, G., Ecker, J., Theologis, A. and Davis, R.W.	CDS	/codon_start=1 /protein_id="AAF02832.1" /db_xref="GI:6056368" /translation="MQEHTTDFKNHTLPLARIKKIMKADEDVRMISAEAPVIFAKA CPMFILLETIRAWITHEENKRTLOKNDIAAIAISRTDVFELVDILPDELKEBGLGV TKGTIPSVVGGSPYYLQQQGMHWPQEQHPDES" /complement(6331..7391) /gene="T6H22.4" /complement(6331..7391) /gene="T6H22.4"
TITLE JOURNAL	Direct Submission Submitted (07-DEC-1999) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA	gene	/note="Putative transcription factor; putative transcription factor. MYB72, R2R3-MYB factor family member. gi13941502" /codon_start=1 /protein_id="AAF02833.1" /db_xref="GI:6056369" /translation="MGKGRAPCCDKNKVGRGWPSPQEDLTITFTQKHGHWRSPLPK LAGLLRCGKSCRLRWVILRPDYKRGNSKKEEDALIHQTLGNKWSKIASFLPGRT DNEIKVWNTHLKKRLTFSSSSLSSTHSDQSTKADHKNCDGAQEEIHSGNESQNS ATSSHQGECHMTKPELHEVNLGNEIQFLDHDHDDITSEFLQDNDILFLDLSLLHN HOTHSHTQEMTREVTKSQSFDPHPQDIPCGFEDTNEESDLRRQLVESTTPNNEYDEWF NFIDNITVDFDFNFVGEVCL" /complement(12011..12343) /gene="T6H22.5" /complement(12011..12343) /gene="T6H22.5"
COMMENT	On Sep 16, 1999 this sequence version replaced gi:5822967. 'IGF' clone F14J16, gb AC002304. e-mail for correspondence: arab@sequence.stanford.edu Genes with similarity to proteins in the databases are described as 'putative', '-like', or 'similar to'. Genes that have EST similarity but no significant protein similarity are described as 'unknown proteins'. Genes that are annotated based only on gene prediction software are described as 'hypothetical proteins'. The software programs used to predict genes include: Grail (Informatics Group, Oak Ridge National Laboratory, http://compbio.ornl.gov/section/index.html), GENSCAN (Chris Burge, http://gnomic.stanford.edu/ chris/GENSCANW.html), Fexa (V.Solovyev & A.Salamov, Sanger Centre, http://genomic.sanger.ac.uk/), and NetPlantGene (S.M. Hebsgaard, et al., CBS, Technical University of Denmark, http://www.cbs.dtu.dk/NetPlantGene.html).	CDS	/note="Unknown protein; Location of ESTs 152M277, gb R84175 and 152M2XP 3 prime, gb AA394633" /codon_start=1 /protein_id="AAF02834.1" /db_xref="GI:6056370" /translation="MKQILRLSRVADSTQVSLRSESGRGTKEKHKSWPGEHVP VYVGHGEMERFVYNAELLNHPVALLKQSAOBYGYEQQGLRIPCHVILVFRILESLR LGADRVTF" /complement(21550..21550) /gene="T6H22.7" Join(15883..15949,16151..16337,16412..16483,16565..16636, 16877..16948,17113..17184,17313..17384,17854..17925, 18077..18148,18446..18511,18783..18844,18955..19331, 19631..19829,19908..20066,20165..20283,20388..20598, 20680..20911,20992..21142,21215..21550) /gene="T6H22.7" /note="Similar to serine/threonine kinases" /codon_start=1
FEATURES source	Location/Qualifiers 1..96489 /organism="Arabidopsis thaliana" /db_xref="taxon:3702" /chromosome="1" /clone="T6H22" complement(<1..1372) /gene="T6H22.1" complement(join(<1..210,460..720,804..881,962..1372)) /gene="T6H22.1" /note="This gene is not complete, it extends beyond the end of this BAC." /codon_start=1 /product="phosphoglycerate kinase" /protein_id="AAF02830.1" /db_xref="GI:6056366" /translation="MASTATAALSIIKSGAAVTRSSRASFCHIPSTSVSARRLGF SAVDSRFVHVASKVHSVRGKARGVITMAKKSVDLNSVDLKGKVFVRADLNPL DDNONTDDTRIAAIPTIKFLIENGAKVILSTHLGRPKGVTPKFSIAPLVPRLSLL GIEVVKADDCIGPEVETLVASLPPEGVLLLENVRFYKEEKNEPDKAKLASLADLY	gene	
CDS		CDS	





<b>TITLE</b> <b>JOURNAL</b>	Direct Submission Submitted (14-APR-2000) Arabidopsis thaliana Genome Center, Department of Biology, University of Pennsylvania, 38th Street and Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA
<b>REFERENCE</b> <b>AUTHORS</b>	5 (bases 1 to 106320) Ecker, J. R.
<b>TITLE</b> <b>JOURNAL</b>	Direct Submission Submitted (13-MAY-2000) Arabidopsis thaliana Genome Center, Department of Biology, University of Pennsylvania, 38th Street and Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA
<b>REFERENCE</b> <b>AUTHORS</b>	6 (bases 1 to 106320) Cheuk, R., Shinn, P., Brooks, S., Buehler, E., Chao, Q., Johnson-Hopson, C., Khan, S., Kim, C., Altafi, H., Bel, B., Chin, C., Chiou, J., Choi, E., Conn, L., Conway, A., Gonzalez, A., Hansen, N., Howing, B., Koo, T., Lam, B., Lee, J., Lenz, C., Li, J., Liu, A., Liu, J., Liu, S., Mukharsky, N., Nguyen, M., Palm, C., Pham, P., Sakano, H., Schwartz, J., Southwick, A., Thaveri, A., Toriumi, M., Vaysberg, M., Yu, G., Davis, R., Federspiel, N., Theologis, A. and Ecker, J.
<b>TITLE</b> <b>JOURNAL</b>	Direct Submission Submitted (28-JUN-2000) Arabidopsis thaliana Genome Center, Department of Biology, University of Pennsylvania, 38th and Hamilton Walk, Philadelphia, PA 19104-6018, USA
<b>COMMENT</b> <b>FEATURES</b>	On May 13, 2000 this sequence version replaced gi:7549540. Location/Qualifiers 1..106320 /organism="Arabidopsis thaliana" /db_xref="taxon:3702" /chromosome="1" /clone="F14J16" Join(455..553,875..1189) /note="hypothetical protein" /codon_start=1 /evidence=not_experimental /product="F14J16.1" /protein_id="AAF79308.1" /db_xref="GI:8778299" /translation="MQIREFCVENSLOKRCIIVVCQYLIICITYYMSTKOSLLNMT LVGRVLIPTAFQKKKNTFLYERIKINLVNLFYICINKNCRKNTDSIYSSEL TNQRLVPLISTVFTTINOKLKKKTFAPRI" complement(join(1278..1618,1713..1887)) /note="hypothetical protein" /codon_start=1 /evidence=not_experimental /product="F14J16.2" /protein_id="AAF79341.1" /db_xref="GI:8778332" /translation="MQLFSPFLFNLYSVKLVCKTNLYSFFLQORIVLKMDSDE KSMKAMKIASAKPGVRSVSIQNDQLVLLGEGIDLAELIRELKKVCMTIITVQA APPOQPPHPMGQVNOPPARRCTCEIPNSGFCGCRSMOPNQVVPSPYPPMLY CRDPTDCCRIL" complement(join(2385..2501,2665..2763,2933..3227, 3290..3928,3985..4183,4476..4630,5451..6164,6220..6499, 6648..6823,6906..6974,7167..7221,7728..8031)) /note="hypothetical protein" /codon_start=1 /evidence=not_experimental /product="F14J16.3" /protein_id="AAF79340.1" /db_xref="GI:8778331" /translation="MFSSSIRILVSGFHTQPLKSPVNSPSVFIYVPKFFNSKSTG TGSRSVMSVEKTSQSDGASRMREKLEPELVIEDVSYOHAGHAKMG SSIVPCLLAWSQGCFSIESPFLSGEAKPSLYFTSTEQVTELSNLRDGDGEVWV KHYSSKHQILLVGEQFSFCSLACFCGSASNTYASSLSDYDKVPVNGKCSFKLDFS CMSEWNPIDPDVVRYKNARINLETKLKGLAFLLHGVDATTLLHPDLRYRRFDRVI FNPFHTGHRKESDQCIQPAATLNLKDFLHGASHMLRADVGHVSHKKNKAPCY WNDELASRCFLVLIQLEAFKKNPCYENKRGDSRCQDPELLGCSFKFRSVA KELYAEKVEKSPRELSTAMNKKHARFEDSSILHLELPCRTRFKRYSLEMNGE LQMWITRFPHYTKESSETRLLQDYAVQASOEPPELSRLRFGVSHGLHNGVR KLIRNSTGESKRLMRQNRNLKIRDSGDDEEVWKYSSNHQILLVGEQFSFSL ATLFGSACISLSDSYDVVRYKKNKSLNLTKLKGLALLHGVDATTLLHPFDLRL YREFDRVIFNPHAGPHGSDSLIRPAAATSRNMCFFVHLVLYFCVCRKRLVFL GPNGASRLLRANGEVHVSHKKNKAPSEWNLELASRCFLVLIQVAFKKNVGYEN KRGDGRRCQDPLLGECSFTKFKFSRAKELYAEKVRSEKRESMYPEALINQPY
<b>CDS</b>	<p>SDHRYRLQTEFEVGSORVPLFDLSYGRYQNLQVQDPLVKSRERTSPDLCCYQERR CLOLEDSSYRSERSLLOQDFPQFTHHROEQFHESTRTRRYSPDIQYIQRMLTST SPFLVAGSEPRHLLCODFQVQASQSELSYSNRSWGSREIYNWEVYLRKMLFSG YGNKVSASWSSSSLSKNGVIYIILFVAVLLEDFHSVNDSELDITWTRGLDNLQIS VCF"</p> <p>join(8720..8773,9069..9338) /note="hypothetical protein" /codon_start=1 /evidence=not_experimental /product="F14J16.4" /protein_id="AAF79309.1" /db_xref="GI:8778300" /translation="MLILFCIIIFYIVASFGSLKSHIYCHNYHVPMQWGYFRKTK KTFTRFPQKPVTAASLSHLSFNAYTYIRYQYILFLISPVFVCASLSLTGNARVS LSLYV" join(9866..10019,10085..10176,10278..10347,10460..10578, 10791..10974,11021..11100,11177..11371,11464..11547, 11621..11741,11789..11849,11919..12151,12242..12327, 12447..12596) /note="unknown protein; similar to ESTs gblT46383.1, gblN96614.1, gblAI730005.1, and gblAI996700.1" /codon_start=1 /evidence=not_experimental /product="F14J16.5" /protein_id="AAF79310.1" /db_xref="GI:8778301" /translation="MASKSDVNIETSSKVFHSGFQMDGLASNRPEQMAEEEHQOP FVIGESRGVAGGAAGKTTCVDMIOQLHDOQAVVYNQDSFYHNVAEVLVRVHDYNF DHPADFTEOLLSMEKLRKQAVDIPNDFKSKNNVPPRRVNPSDVILRGILIF HDPVRDLMMKIFVDAGLSHTKPVNTYVYKSVAYMRCTCICTHEDADVRLARRIKR KLGQHDLCIKYVNLVYIOSTFIRGMHTLRDSTKTHDFIFYSDRKLRLVLRVHGLGH LPTEKQVVTGKLMKKIIPYVNLGELSNHRSVYSGVDFCKLGVSVIRGESME NALRACCKGIKIGKILIHREGDNGQCVLSLITSPNLLTNTGTHQIYEKLPDI SERHVLDPILGTAGNSAVOATRLISLKGVPESNIIFLNLISAPEGVNVVCKFPRI KIYVSETGLNDEFVRVPCMGEGDRCYCTDDE" join(12990..13164,13696..13745,13837..13912,13998..14118, 14217..14320,14419..14740,14908..15157,15251..15628, 15718..16011) /note="hypothetical protein" /codon_start=1 /evidence=not_experimental /product="F14J16.6" /protein_id="AAF79311.1" /db_xref="GI:8778302" /translation="MSSSDGSSRSVSIYHLRKTLOKIREYTKQHSDEDFIVYKDS FNDAEFKREKANGHVTRKREKKEKASPIVPTQPSGRGRNRFASNSYQSSS RNDPHEAQKLLFLDTEHVRKREKKEKASPIVPTQPSGRGRNRFASNSYQSSS PSLISARCSKSDQAEIETASKQGNQSLPKPDVSEQSHVTFPHLQVAKLQNLG TFGSFDSNFKEVSSNGASGGSDSNFESSHGGDDDERESSPTTNGITGVASARFVTE ILSYILIEETSTVSEKDYGLSNSATGAEPVHSDHIVPVEEVPKEEALSNTETQI AYGQEAFLSVGLVPSLSAIGQPVNTAEATQPGNSPPISLVSPDQSSIAAATQ QTNELRQYPPNFPFYGYSPYMPFYIHQFLSPNGIPQOQSYFPOGAALTAFSHAKP VDNTEPNTNPLYLHTSPMVASSIPSTTILNSIHSEKASHLTESAAGIQCQGFNLQ VPMYNLAYQOPLGFPVQAGHGLMGHQPOTQPMASASTYQTLPPPHPTTAMGE PIGHPHIAYOQQAALTNWNNY" complement(join(16511..16739,16880..17104,17226..17722, 17878..18357,18375..18440,18538..18798)) /note="hypothetical protein" /codon_start=1 /evidence=not_experimental /product="F14J16.7" /protein_id="AAF79339.1" /db_xref="GI:8778330" /translation="MEESRDLMTLIESGVSPIGDFTSVSETPPALVSVICAQLLN CDLSPVFTFLSGLCGFSYLCENHAETDCMCLRQLRHPSEDSYRLVRLVERLSI LIDTSASPSDELPSLPERFRICDIAHSVKNLGYINDMSYKCLIVLKEQAFIVPES CDLSPVFTFLSGLCGFSYLCENHAETDCMCLRQLRHPSEDSYRLVRLVERLSI SEGKTLTAGDIAASPKMETFDISDDMMVNEKDETDFDMHQKVEALVDLMTSEK SHSDSLAKNSAVDSSQCTDPDVTDRSDLSLRSCCEENSIEDPRTNYETVE LQNHQDLLEESGSLCSLELELLQMAERLDDKPKGSGLEQLNQQLVYKR CNIMDKQWYEQYIYFKLKAHMSVSTTSGHDGRVWYEMITKYIMSSFDDVRUT LETKLLLDOLHVEEPAKFKRLKTELDLSLEIQKREDREKLYNLELERQV KAAPRKSIIHGKIETIKNSRKLDTDIQRISGRETQLEKKSIOERLHRSYAVVDVME</p>
<b>CDS</b>	
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Southwick,A., (SSP/Stanford) and Seki,M. (RIKEN GSC) contributed equally to this work. Shinozaki,K. (RIKEN GSC) and Davis,R.W. (SSP/Stanford) contributed equally to this work as PIs.

# FEATURES

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ORGANISM Arabidopsis thaliana

# REFERENCE

Shinn,P., Chen,H., Cheuk,R., Kim,C.J., Banh,J., Bowser,L., Carninci,P., Chung,M.K., Goldsmith,A.D., Hayashizaki,Y., Ishida,J., Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J., Lam,B., Lee,J.M., Lin,J., Liu,S.X., Miranda,M., Narusaka,M., Nguyen,M., Palm,C.J., Pham,P.K., Quach,H.L., Sakano,H., Sakurai,T., Satou,M., Seki,M., Southwick,A., Toriumi,M., Yamada,K., Yu,G., Shinozaki,K., Davis,R.W., Theologis,A. and Ecker,J.R.  
Arabidopsis cDNA clones

# TITLE

Unpublished  
2 (bases 1 to 1471)

# JOURNAL

Shinn,P., Chen,H., Cheuk,R., Kim,C.J., Banh,J., Bowser,L., Carninci,P., Chung,M.K., Goldsmith,A.D., Hayashizaki,Y., Ishida,J., Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J., Lam,B., Lee,J.M., Lin,J., Liu,S.X., Miranda,M., Narusaka,M., Nguyen,M., Palm,C.J., Pham,P.K., Quach,H.L., Sakano,H., Sakurai,T., Satou,M., Seki,M., Southwick,A., Toriumi,M., Yamada,K., Yu,G., Shinozaki,K., Davis,R.W., Theologis,A. and Ecker,J.R.

# AUTHORS

Shinn,P., Chen,H., Cheuk,R., Kim,C.J., Banh,J., Bowser,L., Carninci,P., Chung,M.K., Goldsmith,A.D., Hayashizaki,Y., Ishida,J., Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J., Lam,B., Lee,J.M., Lin,J., Liu,S.X., Miranda,M., Narusaka,M., Nguyen,M., Palm,C.J., Pham,P.K., Quach,H.L., Sakano,H., Sakurai,T., Satou,M., Seki,M., Southwick,A., Toriumi,M., Yamada,K., Yu,G., Shinozaki,K., Davis,R.W., Theologis,A. and Ecker,J.R.

# TITLE

Submitted (15-MAR-2001) Salk Institute Genomic Analysis Laboratory (SIGNAL), Plant Biology Laboratory, The Salk Institute for Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

# JOURNAL

RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN Arabidopsis Full-length cDNA') : Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.

# COMMENT

The Salk, Stanford, PGECC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs (RAFL cDNA : 'RIKEN Arabidopsis Full-length cDNA') : Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.

The Salk, Stanford, PGECC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs (RAFL cDNA : 'RIKEN Arabidopsis Full-length cDNA') : Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.

Shinn,P. (SSP/Salk) and Seki,M. (RIKEN GSC) contributed equally to this work. Shinozaki,K. (RIKEN GSC) and Ecker,J.R. (SSP/Salk) contributed equally to this work as PIs.

# FEATURES

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## ORIGIN

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 1 (bases 1 to 1307)  
 Southwick, A., Karlin-Neumann, G., Nguyen, M., Lam, B., Miranda, M., Palm, C.J., Bowser, L., Jones, T., Banh, J., Carninci, P., Chen, H., Cheuk, R., Chung, M.K., Hayashizaki, Y., Ishida, J., Kamiya, A., Kawai, J., Kim, C., Lin, J., Liu, S.X., Narusaka, M., Pham, P., Sakano, H., Sakurai, T., Satou, M., Seki, M., Shinn, P., Yamada, K., Hayashizaki, K., Ecker, J., Theologis, A. and Davis, R.W.  
 Direct Submission  
 Submitted (14-NOV-2001) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA  
 e-mail for correspondence: arab@sequence.stanford.edu

## COMMENT

Riken Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL CDNA: "RIKEN Arabidopsis Full-length cDNA"): Seki, M., Narusaka, M., Ishida, J., Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J., Hayashizaki, Y. and Shinozaki, K.

The Salk, Stanford, PGSC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Nguyen, M.,

Southwick, A., Karlin-Neumann, G., Lam, B., Miranda, M., Palm, C.J., Bowser, L., Jones, T., Banh, J., Chen, H., Cheuk, R., Chung, M.K., Kim, C., Lin, J., Liu, S.X., Pham, P., Sakano, H., Shinn, P., Yamada, K., Ecker, J., Theologis, A. and Davis, R.W.

Southwick, A., (SSP/Stanford) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Davis, R.W. (SSP/Stanford) contributed equally to this work as PIs.

## FEATURES

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QY 482 cgagcggttaaaacgagttgggtcagcgaattccgtctccagatctcatcactc 541

Db 533 AAAGGAGTAAACAAATTTGGTTCATGATGATGATGATGATGATGATGATGATGATGATG 592

QY 542 cccaatcatctctgagctctccaaaggaagacgctggtcttctgtgaggtattccaaag 601

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		Best Local Similarity 63.2%; Pred. No. 7.2e-37;
		Matches 256; Conservative 0; Mismatches 140; Indels 9; Gaps 2;
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QY	190	cgattacttgatgagacgatgccttcacaataatcatcgaccacctcttgtcctgatcca 249
Db	55522	CTACTACTCTGCTCGGAAGTGGTGGAGCGGAGCTTCAACG --GGCGCGCCATCGCGGA 55466
QY	250	agtcagatctcaacaagtgtgagccttggacatcccaaaaatggcatgcgtggaggagaa 309
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QY	310	ggattggatttctacagccaaagacgacgaaaaatcgcacgsggctgagaactaacgc 369
Db	55405	GGATGGTACTTCTACAGCCTCCGACCGCAAGTACCCACGCGGACTCCGCACCAACCG 55346
QY	370	agaacggccaccggatattggaaaagccacgcggcaagagacaacattcttaa -----g 423
Db	55345	CGCCACGGGGCCGGGCTACTTGGAAAGGCCACGGCAAGGACCGCGAGATCGCGACGCCCG 55286

Db	55285	CACGGCGCCCTCGTGGCATGAAGAAGACCTCGTCTTTACCGCGCCGCCGCCAA	55226
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LOCUS			
DEFINITION		Oryza sativa chromosome 6 clone OSJNBA0021N09, *** SEQUENCING IN	HTG 31-JAN-2002
		PROGRESS ***, in ordered pieces.	
ACCESSION	AP004679		
VERSION	AP004679.1	GI:18447938	
KEYWORDS	HTG; HTGS_PHASE2.		
SOURCE	Oryza sativa (cultivar:Nipponbare) DNA, clone:OSJNBA0021N09.		
ORGANISM	Oryza sativa		
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.		
REFERENCE	1 (bases 1 to 157274)		
AUTHORS	Sasaki, T., Matsumoto, T. and Yamamoto, K.		
TITLE	Direct Submission		
JOURNAL	Submitted (30-JAN-2002) Takuji Sasaki, National Institute of Agricultural Sciences, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan		
	(E-mail:tsusakien@affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Fax:81-298-38-7468)		
	NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.		
COMMENT	* NOTE: This is a 'working draft' sequence.		
	* This sequence will be replaced		



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Qy 324 acagccaagaagacgcaaaaaatacgcgacggggctgagaactaacgcagcaacgcccacg 383
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RESULT 15
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DEFINITION
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cds.
AF360201
VERSION
AF360201.1 GI:13430577
KEYWORDS
FLI_CDNA.
SOURCE
thale cress.
ORGANISM
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
1 (bases 1 to 1109)
Yamada,K., Liu,S.X., Sakano,H., Pham,P.K., Banh,J., Chung,M.K.,
Goldsmith,A.D., Lee,J.M., Quach,H.L., Toriumi,M., Yu,G., Bowser,L.,
Carninci,P., Chen,H., Cheuk,R., Hayashizaki,Y., Ishida,J.,
Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J., Kim,C., Lam,B.,
Lin,J., Miranda,M., Narusaka,M., Nguyen,M., Palm,C.J., Sakurai,T.,
Satou,M., Seki,M., Shinn,P., Southwick,A., Shinozaki,K.,
Davis,R.W., Ecker,J.R. and Theologis,A.
Full Length cDNA of gene F10D13_14 (GI:12597796)
Unpublished
2 (bases 1 to 1109)
Yamada,K., Liu,S.X., Sakano,H., Pham,P.K., Banh,J., Chung,M.K.,
Goldsmith,A.D., Lee,J.M., Quach,H.L., Toriumi,M., Yu,G., Bowser,L.,
Carninci,P., Chen,H., Cheuk,R., Hayashizaki,Y., Ishida,J.,
Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J., Kim,C., Lam,B.,
Lin,J., Miranda,M., Narusaka,M., Nguyen,M., Palm,C.J., Sakurai,T.,
Satou,M., Seki,M., Shinn,P., Southwick,A., Shinozaki,K.,
Davis,R.W., Ecker,J.R. and Theologis,A.
Direct Submission
Submitted (13-MAR-2001) Plant Gene Expression Center, 800 Buchanan
Street, Albany, CA 94710, USA
RIKEN Genomic Sciences Center (GSC) members carried out the
collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN
Arabidopsis Full-Length cDNA') : Seki,M., Narusaka,M., Ishida,J.,
Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J.,
Hayashizaki,Y. and Shinozaki,K.

The Salk, Stanford, PGEN (SSP) Consortium members carried out the
sequencing and annotation of the RAFL cDNAs: Yamada,K., Liu,S.X.,
Sakano,H., Pham,P.K., Banh,J., Chung,M.K., Goldsmith,A.D.,
Lee,J.M., Quach,H.L., Toriumi,M., Yu,G., Bowser,L., Chen,H.,
Cheuk,R., Jones,T., Karlin-Neumann,G., Kim,C., Lam,B., Lin,J.,
Miranda,M., Nguyen,M., Palm,C.J., Shinn,P., Southwick,A.,
Davis,R.W., Ecker,J.R. and Theologis,A.

Yamada,K. (SSP/PGEN) and Seki,M. (RIKEN GSC) contributed equally to
this work. Shinozaki,K. (RIKEN GSC) and Theologis,A. (SSP/PGEN)
contributed equally to this work as PIs.
Location/Qualifiers
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Best Local Similarity 59.7%; Pred. No. 1.6e-26;
Matches 276; Conservative 0; Mismatches 180; Indels 6; Gaps 2;

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Search completed: July 15, 2002, 07:43:47
Job time: 3783 sec
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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 15, 2002, 06:40:44 ; Search time 1596.85 seconds  
(without alignments)  
10878.029 Million cell updates/sec

Title: US-09-889-926-1

Perfect score: 1287

Sequence: 1 gtcaccacgcctcgtctt.....aaaaaaaaagggcgccgc 1287

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*

1: em\_estba:\*  
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3: em\_estin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hic:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hic:\*  
12: gb\_gss:\*  
13: em\_gss\_hum:\*  
14: em\_gss\_inv:\*  
15: em\_gss\_pln:\*  
16: em\_gss\_vrt:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	606.4	47.1	608	9 AV540514	AV540514 AV540514
3	540.4	42.0	1142	12 B08263	B08263 F27J24-Sp6.
4	482	37.5	482	9 AV536694	AV536694 AV536694
5	351	27.3	351	9 AV538912	AV538912 AV538912
6	337.6	26.2	1026	12 B10411	B10411 F23117-Sp6
7	312	24.2	1069	12 B11695	B11695 F27J24-Sp6
8	252.6	19.6	739	10 BM112823	BM112823 EST560359
9	229.6	17.8	494	10 B1123181	B1123181 I018P6SP
10	225.2	17.5	640	10 BE554559	BE554559 sp89f05.y
11	217.4	16.9	715	10 BM112826	BM112826 EST560362
12	213.4	16.6	467	10 B112890	B112890 I014P44P
13	212.2	16.5	588	10 BG791220	BG791220 EST560362
14	208.6	16.2	505	9 AW234514	AW234514 sfl5b08.y
15	208	16.2	441	10 BE554923	BE554923 sp8ze11.y
16	204.6	15.9	418	10 B1123635	B1123635 I026P45P
17	204	15.9	466	9 AW685143	AW685143 NF026A09N

18	201.6	15.7	401	10 B1125742	B1125742 I065P37P
19	198.8	15.4	564	10 BF650098	BF650098 NF087H02E
20	197.6	15.4	445	9 AW032569	AW032569 EST276128
21	183.2	14.2	721	10 BE586058	BE586058 Est#8pT7_
22	169.4	13.2	410	9 AW203239	AW203239 sf27f12.y
23	168.4	13.1	594	12 B25594	B25594 F28E15TR IG
24	166.8	13.0	757	10 BG587963	BG587963 EST489738
25	165.8	12.9	700	10 BF635413	BF635413 NF077C03D
26	165.8	12.9	795	12 BH542565	BH542565 B0RP56TF
27	165.2	12.8	843	10 B1308121	B1308121 EST529531
28	161.8	12.6	772	10 BE661301	BE661301 588 GmaxS
29	158.2	12.3	566	10 BE594436	BE594436 P11_33_D0
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31	155.4	12.1	638	9 AV923588	AV923588 AV923588
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33	148.6	11.5	383	9 AA660001	AA660001 EST00051
34	148.2	11.5	405	10 BG510816	BG510816 sac73f07.
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43	140.4	10.9	613	10 BF644336	BF644336 NF063H08E
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#### ALIGNMENTS

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DEFINITION F23117-Sp6.1 IGF Arabidopsis thaliana genomic clone F23117, DNA  
ACCESION B08241  
VERSION B08241.1 GI:20893363  
KEYWORDS GSS.  
SOURCE thale cress.  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.  
REFERENCE 1 (bases 1 to 1132)  
AUTHORS Feng, J., Dewar, K., Buehler, E., Kim, C., Li, Y., Shinn, P., Sun, H. and Ecker, J.  
TITLE BAC End Sequences at ATGC  
JOURNAL Unpublished (1997)  
COMMENT Other\_GSSs: F23117-T7.1, F23117-T7, F23117-Sp6  
Contact: Ecker J.  
Arabidopsis Thaliana Genome Center  
University of Pennsylvania  
Dept. of Biology, University of Pennsylvania, Philadelphia, PA 19104  
Tel: 215-898-9384  
Fax: 215-898-8780  
Email: jecker@atgenome.bio.upenn.edu  
Seq primer: Sp6  
Class: BAC ends  
High quality sequence start: 93  
High quality sequence stop: 846.  
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Matches 658; Conservative 0; Mismatches 53; Indels 1; Gaps 1;

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ACCESSION
  AV540514
VERSION
  AV540514.1 GI:8702272
KEYWORDS
  EST.
SOURCE
  thale cress.
ORGANISM
  Arabidopsis thaliana
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
  Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
  1 (bases 1 to 608)
REFERENCE
  Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
```



## RESULT 3

B08263  
LOCUS  
DEFINITION B08263 1142 bp DNA linear GSS 14-MAY-1997  
F27J24-Sp6.1 IGF Arabidopsis thaliana genomic clone F27J24, DNA  
sequence.  
ACCESSION B08263  
VERSION B08263.1 GI:2089385  
KEYWORDS GSS.  
SOURCE thale cress.  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
1 (bases 1 to 1142)  
Feng, J., Dewar, K., Buehler, E., Kim, C., Li, Y., Shinn, P., Sun, H. and  
Ecker, J.  
BAC End Sequences at ATGC  
Unpublished (1997)  
Other\_GSSs: F27J24-T7, F27J24-Sp6  
Contact: Ecker J.  
Arabidopsis Thaliana Genome Center  
University of Pennsylvania  
Dept. of Biology, University of Pennsylvania, Philadelphia, PA  
19104  
Tel: 215-898-9384  
Fax: 215-898-8780  
Email: jecker@genome.bio.upenn.edu  
Seq primer: Sp6  
Class: BAC ends  
High quality sequence start: 87  
High quality sequence stop: 816.  
Location/Qualifiers  
1. .1142  
/organism="Arabidopsis thaliana"  
/strain="Columbia"  
/db\_xref="taxon:3702"  
/clone="F27J24"  
/clone\_lib="IGF"  
/sex="hermaphrodite"  
/note="Vector: BelobACII; Site\_1: EcoRI; Site\_2: EcoRI;  
Produced by Thomas Altmann"

## FEATURES

Source

BASE COUNT 310 a 282 c 217 g 331 t 2 others  
ORIGIN  
Query Match 42.0%; Score 540.4; DB 12; Length 1142;  
Best Local Similarity 90.3%; Pred. No. 1.9e-86;  
Matches 645; Conservative 0; Mismatches 61; Indels 8; Gaps 6;  
QY 567 aggaagactgggtctgtgttaggtattccataagaatacgaagaggttatgtagag 626  
DB 263 AGGAGACTGGGTCTGTGTAGGTATTCCATAAGAATACGGAAGGTTATATGTAGAG 322  
QY 627 acaacatggaagctgtttgtatgacagacctgtcatcgcttctccactgatgatc 686  
DB 323 ACAACATGGAAGCTGTTTGTATGAGACAGCCTCTGCATCGCTTCTCCACTGTATGATC 382  
QY 687 cttacatcaactttgaccagaacctcttcttctcagtgatgatcatcactacatca 746  
DB 383 CTTACATCAACTTTGACCAAGAACCTCTTCTATCTCAGTGATCATCATCATCATCA 442  
QY 747 tcaatgagcacgtaccctgtcttctccaatttgtcacagaaaccccttaactgaacc 806  
DB 443 TCAATGAGCACGTACCCCTGTTCTCCAAATTTGTCACAGAACCAACCTTAAACTCGAAC 502  
QY 807 taaccaactcagctctgaactcaagattccatgcaagaaccttaacctgtttactg 866  
DB 503 TAACCAACTCAGTCTCTGAACCTCAGATTCAGATTCCTATGCAAGAACCTTAACCCCTGTTTACTG 562  
QY 867 gtgggtcagctccagccagctccagccctcagctcattctgtcttcagatcagatgg 926  
DB 563 GTGGGTCAGCCTCAGCCAGGCTCACAGGCTCGACTCATCTGTTCTTCAGATCATGATGG 622

QY 927 ttctcagagcttactcagctcagctcactaagattggaagctcgggcctaagaat 986  
DB 623 TTCTCAAGCCTTACTCTAGTCAGCTCACTAAGATTGATGGAG-CTCGGGCTAAAGAAT 681  
QY 987 cacagagttatggagaaggtagctcgagagcctctgacccagatcggtattccaaagca 1046  
DB 682 CACAGAGTTATGGAGAAAGGTACTCGGATAGCTTCTTCCACCGACATCGTATCCCAACCA 741  
QY 1047 ctggttgaattgctgatgacgagtgtaacgagaggttactattgctatatctctatoca 1106  
DB 742 CGGTTGGGAA-TGCTGATGATCGA-TGTTACGAGAGTTACTATTGCTATATTCCTACTCA 799  
QY 1107 tgattggacaattcttcggggggaataacggtgctgtctgctgatgtacaaacatttc 1166  
DB 800 TGA-TGGAAATACTCTCGGGGGGATATAACGTTTGTGCTGCTGAATGTACAAACTTTTC 858  
QY 1167 ctactctgtaccac-ggtagattcatgtataat---accacttatgacgtagacat 1222  
DB 859 CTCACCTCTGTACCCCGGGTAGATTTCATGTTAAATTACCCCTTTTGAACGCCAGAACCT 918  
QY 1223 acatatattcatgtagtcttcatttggtttcacacacacacacacacacacacacacacac 1276  
DB 919 CTTATTTTCCAACGTAATTCCTATTTTGTTCAGGGTTATAAGGACCTCTATAAAA 972

## RESULT 4

AV536694  
LOCUS AV536694 482 bp mRNA linear EST 06-SEP-2000  
DEFINITION AV536694 Arabidopsis thaliana liquid-cultured seedlings Columbia  
Arabidopsis thaliana cDNA clone PAZNI10438R 5', mRNA sequence.  
ACCESSION AV536694  
VERSION AV536694.1 GI:8696977  
KEYWORDS EST.  
SOURCE thale cress.  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
1 (bases 1 to 482)  
Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.  
A large scale analysis of cDNA in Arabidopsis thaliana: Generation  
of 12,028 non-redundant expressed sequence tags from normalized and  
size-selected cDNA libraries  
DNA Res. 7, 175-180 (2000)  
20363093  
Contact: Erika Asamizu  
The First Laboratory for Plant Gene Research  
Kazusa DNA Research Institute  
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan  
Email: asamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.  
Location/Qualifiers  
1. .482  
/organism="Arabidopsis thaliana"  
/strain="Columbia"  
/db\_xref="taxon:3702"  
/clone="PAZNI10438R"  
/clone\_lib="Arabidopsis thaliana liquid-cultured seedlings  
Columbia"  
/tissue\_type="liquid-cultured seedlings"  
/note="Vector: pBluescriptII SK-; Site\_1: EcoRI; Site\_2:  
Xhoi"

## FEATURES

BASE COUNT 160 a 104 c 123 g 95 t  
ORIGIN  
Query Match 37.5%; Score 482; DB 9; Length 482;  
Best Local Similarity 100.0%; Pred. No. 5.7e-76;  
Matches 482; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 33 cctcttaacctcactaatcaaacactaaacctagaaaaaaagggatcaaatatgg 92  
DB 1 CCTCTTAACCATCCACTAATCAACACTAGAAAAAAGGATCAATCATG 60



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Query Match      26.2%; Score 337.6; DB 12; Length 1026;
Best Local Similarity 85.6%; Pred. No. 1.7e-50;
Matches 375; Conservative 0; Mismatches 62; Indels 1; Gaps 1;

QY 567 aggaagactgggtctgttagggattccataagaatacgaagagaggttatgtatag 626
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 309 ANGAATACTGGTTCTGTGTANGTATCCCATANAATAACGAAGAGTTATATGTAAG 368

QY 627 acaatgggaagctgtttgatgagacagctctcatcgtctccctccactgatgac 686
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 369 AACACATGGGAAGCTGTTTGTATGAGACAGCCCTCTGCATCGCTCCCTCCACTGATGATT 428

QY 687 ctatcatcaactttgacccaagaacctctcttatctcatcagtgatgatcatcatcata 746
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 429 CTTACATCAACTTTGAACCAAGAACCTCTTCTNATCTCAGTGATGATCATCATCATCA 488

QY 747 tcaatgagacgtaccctgtcttccaatgttgcacagaacccaaccttaacctgaacc 806
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 489 TCAATGAGCAGCTACCCCTCTCTCCANTTGTACAGAAACANACCTTANACTCGAAAC 548

QY 807 taaccaactcagtcctgtgaactcaagattccatgcaagaacccctaacctctgttactg 866
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 549 TANCNACTCAGTCTGAAACTCAGAAATCCCATGCAGAACCTTAACCCCTGTNACTG 608

QY 867 gtggttcagcctcagccagctcacagggcctcagctcattctgttctcagatcagatgg 926
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 609 GTGTTTCAGCCTCAGCCAGCTCAGAGGCTCGACTCANCTCTGTCTTCAGATCAATNN 668

QY 927 ttctcagagctctactcagtcagctcactaagattgatgaagccctcggcctaaagaat 986
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 669 GTCTCAAAAGCTCTACTCAGTCAGCTACTNAGAATGATGAAGCCCTCCCGCCT-AAGAAT 727

QY 987 cacagagttatggagaag 1004
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 728 CACNAATTTATGAAGG 745

RESULT 7
B11695      1069 bp      DNA      linear      GSS 14-MAY-1997
LOCUS       F27J24-Sp6 IGF Arabidopsis thaliana genomic clone F27J24, DNA
DEFINITION sequence.
ACCESSION  B11695
VERSION    B11695.1 GI:2092828
KEYWORDS   GSS.
SOURCE     thale cress.
ORGANISM   Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE  1 (bases 1 to 1069)
AUTHORS    Feng, J., Dewar, K., Buehler, E., Kim, C., Li, Y., Shinn, P., Sun, H. and
            Ecker, J.
            BAC End Sequences at ATGC
            Unpublished (1997)
            Other_GSSs: F27J24-Sp6.1, F27J24-T7
            Contact: Ecker, J.
            Arabidopsis Thaliana Genome Center
            University of Pennsylvania
            Dept. of Biology, University of Pennsylvania, Philadelphia, PA
            19104
            Tel: 215-898-9384
            Fax: 215-898-8780
            Email: jecker@genome.bio.upenn.edu
            Seq primer: Sp6
            Class: BAC ends
            High quality sequence start: 475
            High quality sequence stop: 490.
            Location/Qualifiers
                source          1..1069
                                /organism="Arabidopsis thaliana"
                                /strain="Columbia"
                                /db_xref="taxon:3702"
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/clone="F27J24"
/clone_lib="IGF"
/sex="hermaphrodite"
/nt="Vector: BelOACII; Site_1: EcoRI; Site_2: EcoRI;
Produced by Thomas Altmann"
BASE COUNT 355 a 235 c 20 g 360 t 99 others
ORIGIN

Query Match      24.2%; Score 312; DB 12; Length 1069;
Best Local Similarity 69.7%; Pred. No. 5.9e-46;
Matches 424; Conservative 0; Mismatches 182; Indels 2; Gaps 2;

QY 567 aggaagactgggtctgttagggattccataagaatacgaagaggttatgtatag 626
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Db 303 ANNAATAATNNTCTTTTANNNTATCCATAAAATACNAANAATAATATATATATAA 362

QY 627 acaatgggaagctgtttgatgagacagctctcagtcagtcagtcagtcagtcagtcagtc 686
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 363 ACAACATNNNAACCTTTTAAATAAAACACCTCTNCATCNCCTTCTCCACTAATNAAT 422

QY 687 ctatcatcaactttgacccaagaacctctcttatctcagtcagtcagtcagtcagtcagtc 746
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 423 CTTACATCAACTTTAAACAAACAAACCTCTCTTATCTCATTAATTAATCATCATCATCA 482

QY 747 tcaatgagacgtaccctgtcttccaatgttgcacagaacccaaccttaacctgaacc 806
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 483 TCAATAAACACATTACCTNCTTCTCTAATTTTTCACAAAAACAAACCTTATACTCAAA 542

QY 807 taaccaactcagtcctcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtc 866
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 543 TAACCAACTCATCTCTAAACTCAAAATCCATNCAAAACCTTCTTTTACTN 602

QY 867 gtggttcagcctcagccagctcacagggcctcagctcattctgttctcagatcagatgg 926
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 603 TTTTTCACACCTCAACNACNCTTACANACCTTAATTAATCTTTCTTCAATCAATCAATN 562

QY 927 ttctcagagctctactcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtc 986
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 663 TTCTCAAACTCTACTTCTATCNCCTCATTAATAATNTATCNAACCTTCCNCCCTTNAAT 722

QY 987 cacagagttatggagaagtagctcggagagcctcctcagcagacatcggtattccaaaga 1046
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 723 CACA-AAATATTNAAAAATTTCTCCAAACCTCTTCAACCAACTCTTTATTTCAACCA 781

QY 1047 ctggttggaatgtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtc 1106
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 782 CTTTTCATAAATTTAAATTAATCAAAATTAAC-AAATTAATTAATTTAAATTTCTATTC 840

QY 1107 tgattggaacaattcttcggggggaataaacgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1166
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 841 TAAATTAACAACTTTCCNANNAATAAACTTTCTTTCTTAAATTTCCAAAAATTTCTCT 900

QY 1167 ctcaactct 1174
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Db 901 CTCCTTTT 908

RESULT 8
B112823
LOCUS       B112823
DEFINITION EST560359 potato roots Solanum tuberosum cDNA clone cPRO16A9 5' end
            , mRNA sequence.
ACCESSION  B112823
VERSION    B112823.1 GI:17075871
KEYWORDS   EST.
SOURCE     potato.
ORGANISM   Solanum tuberosum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
REFERENCE  1 (bases 1 to 739)
AUTHORS    van der Hoeven, R., Sun, H., Karamycheva, S.A., Tsai, J., Van Aken, S.,
```





sequencing. The Institute for Genomic Research. Roots were isolated from in vitro grown stem cuttings on CM medium. Roots were isolated two weeks after placing the stem cuttings from in vitro grown plants on medium."

BASE COUNT 242 a 153 c 134 g 186 t  
ORIGIN

Query Match 16.9%; Score 217.4; DB 10; Length 715;  
Best Local Similarity 67.3%; Pred. No. 4e-29;  
Matches 368; Conservative 0; Mismatches 171; Indels 8; Gaps 4;

Qy 100 agagagatgaagaagttagtataagcattggtgaggaagaaagtgctccgggattcag 159  
Db 16 AAAAAATGAGTAACAAACAGCAGCTTTCAGCATGGTGAATCCAAATTAACCAACGAGATTAG 75  
Qy 160 attcaccggaagacacatgctgtcgtgattcctgattcgtatgagacgattcctca--- 216  
Db 76 ATTTCATCCAGAGATGAAGAACCTTATTGTGATTACTTAATGAAGAAAGTTGATCAATC 135  
Qy 217 caataatcatgaccacacctctgtcctgattcccaagtcgattcacaagaagtgtgagccttg 276  
Db 136 CACAGACCAACAACAATACCTCTCTCATAGAAAGTTGACCTCAATAAATCCGAACCTTG 195  
Qy 277 ggacatccccaaaaatggcattgctggtgaggaaggattgttattctacagccaaagaga 336  
Db 196 GGAATTTCTTGAAGTGCATGTGTTGGAGGCAAGGATTGTTACTTCTACAGCCCAAGCTGA 255  
Qy 337 ccgaaatacgcagcggcgtggaactaacacagcaacgcccacggatattggaaagc 396  
Db 256 CCGAATATAGCGAGCGGGTCCGAACAACAGAGCCACCGTATCTGTTACTTGGAAAGC 315  
Qy 397 caccggcaagacagacacattcttaagaaagggtaagcttagttgggattgagggaagacatt 456  
Db 316 CACCGAAAGAGATCGTCAATAATACAGAAAGGAAGCTTGTAGGAATGAGGAA-ACCCT 374  
Qy 457 ggtttctatcaagtgagcctcctgagcgttaaaacgattggtggtcatgcacgaatt 516  
Db 375 AGTTTTCTATCAGGAAGAGC-CCCAAGGAAGAAAGATGTTGCTGTTTATGATCAAT 433  
Qy 517 ccgtctccaggattctcatcctcccaatcattctc---tgagctctcccaaggaaga 573  
Db 434 CCGCTTTGATGAAGGTCCTTAGTAACATTCGTTCTCAATTTCTCTCAAGGAGGA 493  
Qy 574 ctgggtcttctgtaggtattccataaatacgggaaggatttatgttagagacaacat 633  
Db 494 TTGGGTATTATCGCGAGTATTTTCAAGAACAAAGAAATTAATTGCTTACCAAGCAGGGAAT 553  
Qy 634 gggaagc 640  
Db 554 TGGNAGC 560

RESULT 12  
BI122890  
LOCUS 467 bp mRNA linear EST 31-DEC-2001  
DEFINITION BI122890 Populus leaf cDNA library Populus tremula x Populus tremuloides cDNA, mRNA sequence.  
ACCESSION BI122890  
VERSION BI122890.1 GI:18006865  
KEYWORDS EST.  
SOURCE Populus tremula x Populus tremuloides.

ORGANISM Populus tremula x Populus tremuloides.  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Malpighiales; Salicaceae; Populus.  
REFERENCE 1 (bases 1 to 467)  
AUTHORS Hertzberg, M., Aspeborg, H., Erlandsson, R., Bjorkbacka, H., Hiltonen, T., Karlsson, J., Teeri, T., Gustafsson, P., Bahler, R., Jansson, S., Nilsson, O., Sundberg, B., Nilsson, P., Uhlen, M., Sandberg, G. and Lundberg, J.  
TITLE Gene expression in Populus  
JOURNAL Unpublished (2001)

## COMMENT

Contact: Erlandsson R  
Department of Biotechnology  
Royal Institute of Technology  
Teknikringen 30, Stockholm S-10044, Sweden  
Tel: 46 8 790 8287  
Fax: 46 8 245452  
Email: rikeri@biochem.kth.se.

## FEATURES

source 1..467  
/organism="Populus tremula x Populus tremuloides"  
/db\_xref="taxon:47664"  
/clone\_lib="Populus leaf cDNA library"  
/note="organ: leaf"  
BASE COUNT 142 a 93 c 120 g 112 t  
ORIGIN

Query Match 16.6%; Score 213.4; DB 10; Length 467;  
Best Local Similarity 74.0%; Pred. NO. 2.4e-28;  
Matches 301; Conservative 0; Mismatches 96; Indels 10; Gaps 2;  
Qy 105 agatgaagaagaagttagtataagcattggtgaggaagaaagtgctccgggattcagatttc 164  
Db 69 AGAGAAAAGATGAGCAACATAAGCTTTCGTGGAGGCAAAAACGCCACGAGGTTAGGTTC 128  
Qy 165 acccgaagaagcattgagctgtctgctgattcctgattcgtatgagcgtctcacaataatc 224  
Db 129 ATCCAAGAGATGAAGAGCTTGTATGTGATTACTTGATGA-----AGAAGGCTTCTC 179  
Qy 225 atcgaccaccttctcctgatcccaagtcgattcacaagaagtgtgagccttgggacatcc 284  
Db 180 ACTGGGACTCCCTTCTCATGTAGAGGTGACCTCAACAAGTGTGAGCTTGGGATATTC 239  
Qy 285 caaaatggcattggtgaggaagattgttattctacagcaaaagacgaaat 344  
Db 240 CTGAAACCGCATGCGTGGAGCAAGGAATGTTACTTTTACAGCCAAAGAGATCGTAAT 299  
Qy 345 acgc-gacggggctgagaactaacccgagcaacgagcggccacggatattggaagccacggc 403  
Db 300 ATGCAGACTGGACTAAGAACTAATCGAGCAACAGCATCTGGATATTGGAAGCCACCGGT 359  
Qy 404 aaagacagaaccattcctaagaaggtaagcttagttgggattgaggaagacattggttttc 463  
Db 360 AAGGACACACATATCTCTACGTAAGGGAACCCCTTTTGGCATGAGAAAGACCTTGTGTT 419  
Qy 464 tctcaggtcagctcctcggagccgtaaaacggattgggtcgtgca 510  
Db 420 TACCAAGTAGGGCACCCTTAAGGGGNAACCAACCGATTGGGTAAATGCA 466

## RESULT 13

BI122890  
LOCUS 588 bp mRNA linear EST 16-MAY-2001  
DEFINITION ESTFNL083 Tomato Root Subtraction cDNA Library Lycopersicon esculentum cDNA clone 10G5 5' similar to NAC1, mRNA sequence.  
ACCESSION BI122890  
VERSION BI122890.1 GI:14126782  
KEYWORDS EST.  
SOURCE tomato.  
ORGANISM Lycopersicon esculentum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum; Lycopersicon.

REFERENCE 1 (bases 1 to 588)  
AUTHORS Wang, Y.-H., Garvin, D.F. and Kochian, L.V.  
TITLE Nitrate-induced genes in tomato roots. array analysis reveals novel genes that may play a role in nitrogen nutrition  
JOURNAL Plant Physiol. 127 (1), 345-359 (2001)  
MEDLINE 21437959  
COMMENT Contact: Kochian LV  
US Plant Soil & Nutrition Lab  
Cornell University

A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wyllie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterson, R. and Wilson, R.

**TITLE** Public Soybean EST Project  
**JOURNAL** Unpublished (1999)  
**COMMENT** Contact: Shoemaker R/Public Soybean EST Project  
Public Soybean EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63110  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu

This clone is available through: ResGen, Invitrogen Corp. 2130 South Memorial Parkway Huntsville, AL 35801 For further information call: (800)-533-4363 or contact via email: ccu@resgen.com High quality sequence stock: 330.

Location/Qualifiers  
1. .505

```

1. .505
/organism="Glycine max"
/db xref="taxon:3847"

```

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/clone_lib="Gm-cl028"
/tissue_type="roots of 'Supernod' plants"
/lab_host="DH10B"
/notes="Vector: pBluescript II XR; Site_1: EcoRI; Site_2:
XhoI; The mRNA was isolated from roots of Glycine max
'Supernod' plants generously donated by Dr. Gary Stacey.
The seedlings were inoculated with Bradyrhizobium
japonicus, strain USDA110 prior to harvest. Stratagene's
cDNA synthesis kit (catalog number 200401) was used to
synthesize the cDNA. First-strand synthesis was performed
with 5-methyl dCTP, hence the ligated cDNA was
hemimethylated. A modification of Stratagene's
first-strand synthesis primer was used. An 'anchor'
nucleotide (V=A,C, or G) was added to the 3' end of the
primer [GAGAGAGAGAGAGAGACTGCTCGAG(T)18V] to anchor
the primer at the 5' end of the poly(A) tract. After
second-strand synthesis, the cDNA ends were filled in with
cloned Pfu DNA polymerase, ligated to EcoRI adapters and
subsequently phosphorylated. The XhoI site within the
first-strand synthesis primer was then restricted by
digestion with XhoI; all XhoI sites in the cDNA would be
protected by their hemimethylated status. The cDNA
constructs were size-fractionated with a 500bp cutoff,
using GibcoBRL Life Technologies' cDNA Size Fractionation
column. The column eluent was then ligated into
Stratagene's pBluescript II XR predigested vector
(pBluescript II SK(+)) that has been digested with EcoRI
and XhoI, and phosphorylated by Stratagene). Both the
white and blue colonies appear to contain recombinant
plasmids with cDNA inserts, based on size (n=25). This
library was constructed by Dr. Paul Keim and Dr. Virginia

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	BASE COUNT	149 G	105 C	110 A	157 T	
ORIGIN						
Query Match			16.2%;	Score 208.6;	DB 9;	Length 505;
Best Local Similarity			71.3%;	Pred. No. 1.6e-27;		
Matches 293; Conservative			0;	Mismatches 109;	Indels 9;	Gaps 1;
QY	116	a g t a g t a a g c a t g t g g a g g c a a a g t t c c t c c g g g a t t c a g a t t t c c c g a a g a c	175			
D b	104	A G C A A C A A C A T G G T A C A G G C A A A G C T C C A C C A G G A T T C A G G T T T C A C C A A G A G A T	163			
QY	176	g a t g a g c t t g t c t g c g a t t a c t i g a t g a g c a t c g t c c a c a a t a a t c a t c g a c c a c c t	235			
D b	164	G A G A G C T T G T G T G A T T A C T T G A T G A A G A A G G T G C A A C A C A A T G A T - - - - - - - - - - T C C	214			
QY	236	c t t g t c c t g a t c c a a g t c g a t c t c a c a a g t g t g a g c c t t g g a c a t c c c c a a a a t g g c a	295			



Db 215 CTTCTCTTGATAGATGTTGACCTTAACAAGTGTGACCCATGGGATATTCTTGAACAGCA 274

QY 296 tgcgtggagggaagattggtattttctacagccaaagagacgaataacgcgacgggg 355

Db 275 TGGCTTTGGAGGGAAGGAGTGTATTTCTACACAAAGAGAGCGTAAGTATGATCAACACGG 334

QY 356 ctgagaactaacgaacgaacggccacggatattgaaagccacacggcgaagacagaacc 415

Db 335 TTACTCACAATCGTCCACTGCCTCAAGGTATTTGAAGGCCACATGGAAGACAGGCGCT 394

QY 416 attctaagaagggttaagctagttggtgaggaagacacattggttttctatcaaggtcga 475

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RESULT 15

BE554923

LOCUS

DEFINITION

sp82e11.y1 Gm-cl045 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-cl045-165 5' similar to TR:004017 O04017 CUC2. ; mRNA sequence.

ACCESSION

BE554923

VERSION

BE554923.1 GI:9819410

KEYWORDS

EST.

SOURCE

soybean.

ORGANISM

Glycine max

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.

1 (bases 1 to 441)

Shoemaker, R., Keim, P., Vodkin, L., Erpelting, J., Coryell, V., Khanna, A., Bolla, B., Marria, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.

Public Soybean EST Project

Unpublished (1999)

Contact: Shoemaker R/Public Soybean EST Project

Public Soybean EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available through: ResGen, Invitrogen Corp. 2130 South Memorial Parkway Huntsville, AL 35801 For further information call: (800)-533-4363 or contact via email: ccu@resgen.com

Insert Length: 1106 Std Error: 0.00

High quality sequence stop: 419.

Location/Qualifiers

1..441

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/clone="GENOME SYSTEMS CLONE ID: Gm-cl045-165"

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/note="Vector: pBluescriptII SK+; Site\_1: EcoRI; Site\_2: XhoI; This cDNA library was constructed from mRNA isolated from etiolated hypocotyl tissue of 9-10 day old seedlings of the cultivar Williams 82. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) primer with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by digestion with EcoRI and XhoI. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells

## FEATURES

## Source

(Gibco BRL). This library was constructed by Dr. Randy Shoemaker.

BASE COUNT 139 a 85 c 117 g 98 t 2 others

Query Match 16.28; Score 208; DB 10; Length 441;

Best Local Similarity 72.7%; Pred. No. 2.2e-27;

Matches 298; Conservative 0; Mismatches 102; Indels 10; Gaps 2;

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QY 176 gatgagcttgcgtgcgattactgtatgagacgattcgttcacaaataatcatcgaccacct 235

Db 102 GAAGAGCTTGTGTGTGATTACTTGTATGAAGAAGGTGCAACACAAATGAT-----TCC 152

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QY 356 ctgagaactaacgagcaacggccacggatatttgaaagccacccggcgaagacagaacc 415

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QY 416 attctaagaagggttaagctagttggtgaggaagacattggtttctatcaaggtcga 475

Db 333 ATCTCCGCAAGGCGACCCATGTTAGGNATGAGAAAAGAC-TTGGTGTTCATATCAAGGAAGG 391

QY 476 gctcctcagagccgttaaaacccgattgggtcattgcacgaattccgtctcca 525

Db 392 GCACCCAAAGGGAAGAAAACACTGAGTGGGTGTCATGCATGAGTTCGTATCGA 441

Search completed: July 15, 2002, 07:07:53

Job time: 1629 sec





GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 15, 2002, 06:40:44 ; Search time 199.27 seconds  
(without alignments)  
11088.819 Million cell updates/sec

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Perfect score: 1287  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues  
Total number of hits satisfying chosen parameters: 3472872

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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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PR 26-OCT-1999;	99US-0161361.
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PR 28-OCT-1999;	99US-0161993.
PR 29-OCT-1999;	99US-0162142.
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Qy 138	caaaagtgcctccgggattcagatttcacccgaagggagcatgagctgtctgcgattact 197
Db	
186	tagatctaccacaggattcagatttcacccctactgatgaagaac---tcataactcact 242
Qy 198	tgatgagacgatcgcttcacataatcatcacacaccttctctgctactggtgaattggt 257
Db	
243	acctcaaaccaagggtttcaacaccttctctgctactggtgaattggtgactgact 302
Qy 258	tcacaagtgtgagccttgggacatcccaaaatggcatgcgtgggagggaggaattggt 317
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303	tcacaagtgtgagccttgggacttaccatggaaggctaaagatgggagaaagaatggt 362
Qy 318	attctacagccaaagagacgcgaataacgcgcagcggggctgagaaactaacgcgcaacgg 377
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Qy 438	ttgggatgaggaagacattggtttctatcaaggctcagctcctcgagccgtaaaacgg 497
Db	
483	tggtgatgaagaaacttggttttctataaaggaagagctcctaaaggagtaaaacca 542
Qy 498	attgggtcatgcacgaattccgtctccaaaggatctcatcctccatctctctcttctga 557
Db	
543	attgggttatgcatgaatcgttttagaaggcgaataatgtattgaaatcttccccaaa 602
Qy 558	gctctccaaaggaagactgggtctgtgtagggtattccataagaataacggaagg 612
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AC	AAC49011;
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DT	18-OCT-2000 (first entry)



XX Arabidopsis thaliana DNA fragment SEQ ID NO: 59596.  
XX Hybridisation assay; genetic mapping; gene expression control;  
KW protein identification; signal transduction pathway;  
KW metabolic pathway; promoter; termination sequence; ss.  
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XX Arabidopsis thaliana.  
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XX EPI033405-A2.  
XX  
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XX 27-AUG-1999; 99US-0151066.



CC plants environmental stress. The transcription factor is encoded by  
 CC environmental stress tolerance gene derived from Arabidopsis thaliana.  
 CC The transcription factors and the genes encoding them are used to alter  
 CC the structure and developmental characteristics of plants such as  
 CC soybean, wheat, corn, potato, cotton, rice, oilseed rape, sunflower,  
 CC alfalfa, sugarcane, turf, banana, blackberry, blueberry, strawberry,  
 CC raspberry, cantaloupe, carrot, cauliflower, coffee, onion, cucumber,  
 CC eggplant, grapes, honey dew, lettuce, mango, melon, papaya, peas,  
 CC peppers, pineapple, spinach, squash, sweet corn, tobacco, tomato,  
 CC watermelon, roseaceous fruits and/or vegetable brassicas. These sequences  
 CC are also used for modifying traits associated with environmental stress  
 CC tolerance, such as freezing, chilling, heat, drought, water saturation,  
 CC salt, photoconditions, radiation and ozone. The transcription factors  
 CC are used in gene therapy.

XX Sequence 1481 BP; 475 A; 266 C; 310 G; 430 T; 0 other;

Query Match 13.3%; Score 171.8; DB 22; Length 1481;  
 Best Local Similarity 62.6%; Pred. No. 6.6e-38;  
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 DB 256 aggtttcatccaacagacagatcataacatgttaccttaag---gagaaggtttta 312  
 QY 218 aataatcatcgacacactctgtctctgataccaagtcgataccaagtgtagccttgg 277  
 DB 313 aacagcgcattcagctgtggtcgcattggagagctgataccaagtgtagccttgg 372  
 QY 278 gacatcccaaaatgcatcgctggagaggaagattgtattctacagccaaagagac 337  
 DB 373 gatttgccaagaggccaaagatcggggagagaagattctactctctctcaagggac 432  
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 QY 515 ttcctgtccaaggtatcctatcctcccaatcattctctgagctctcccaaggaagac 574  
 DB 613 tatcgtcttgaaggcaaatattcgtattacaatc---tcccaaaatctgaagggaacgaa 669  
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 DB 670 tgggtcgtgtagggtttttcacagaaca 700

## RESULT 10

AAC40830  
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XX AC AAC40830;

XX DT 17-OCT-2000 (first entry)

XX DE Arabidopsis thaliana DNA fragment SEQ ID NO: 29692.

XX KW Hybridisation assay; genetic mapping; gene expression control;

KW protein identification; signal transduction pathway;

KW metabolic pathway; promoter; termination sequence; ss.

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OS Arabidopsis thaliana.  
 XX BP1033405-A2.  
 XX 06-SEP-2000.  
 PD 25-FEB-2000; 2000EP-0301439.  
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 PR 29-MAR-1999; 99US-0126785.  
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Query Match 12.68; Score 162; DB 21; Length 1321;
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DB 271 cactatctccataagaagggttcttgacacca---gcttcagctaaagctatcggtgaa 327
QY 251 gtcgatctcaacaagtgtgaccttgggacatcccaaaatggcatgcgtgggagggaag 310
DB 328 gttgatttaacaaatcagacgatggaggttaccatgattggcgaataatgggtgagaaa 387
QY 311 gattggtattttacagcacaagacacgaataatcgcgcgaggggctgagaaactaaccca 370
DB 388 gaatggtatttttctgtgtgagagacagaagatccaccgggtttaagaactaaccca 447
QY 371 gcaacggccacggatattggaaagccacccggcgaagacagacacacattcttaagaaaggt 430
DB 448 gcaactgaagccggtattgggaagcggacccgggaagataaagagataaccggggcga 507
QY 431 aagctagttggatgagaaagacattggtttctatcaaggtcgagctcctcagggccgt 490
DB 508 tcaattgttggtatgaagaagacactgtttctatagaggagagctcctaaaggtcag 567
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Db 568 aaacccaaaggtggtgatcatgagctacagcttgaagga---aaattctgtgcccataac 624  
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DT 17-OCT-2000 (first entry)  
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KW Hybridisation assay; genetic mapping; gene expression control;  
KW protein identification; signal transduction pathway;  
KW metabolic pathway; promoter; termination sequence; ss.  
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QY 311 gattggtatttctacagccaaagagacgaaataacgcgacgggggtgagaaactaacga 370  
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QY 491 aaaaccgattgggtcagcagcaattccgtctccaaaggatctcatcctcccaatcat 550  
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XX 18-OCT-2000 (first entry)  
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XX Hybridisation assay; genetic mapping; gene expression control;  
XX protein identification; signal transduction pathway;  
XX metabolic pathway; promoter; termination sequence; ss.  
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XX EPI033405-A2.  
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XX 25-FEB-2000; 2000EP-0301439.  
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XX 05-MAR-1999; 99US-0123180.  
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PR	08-JUL-1999;	99US-0142803.	PR	24-SEP-1999;	99US-0155659.	QY	251	gtcgatctcaacaagtgtgagccttgaggacatcccaaaaatggcatcgctggagggaag	310		
PR	09-JUL-1999;	99US-0142320.	PR	28-SEP-1999;	99US-0156458.	Db	328	gttgatttaacaaatcagagccatgggttaccatggatggcaaaaatgggtgagaaa	387		
PR	12-JUL-1999;	99US-0142977.	QY	04-OCT-1999;	99US-0157117.	QY	311	gattggatttctacagccaaagagaccgcaaaatacgcgcggggctgagactaacga	370		
PR	13-JUL-1999;	99US-0143542.	PR	05-OCT-1999;	99US-0157753.	Db	388	gaatggattttttctgtgtgagagacagaagaagtatccacacgggtttaagaactaacga	447		
PR	14-JUL-1999;	99US-0143624.	PR	06-OCT-1999;	99US-0157865.	QY	371	gcaacggccaccgggatatttgaaagccaccgccaagacagacaccatttctaagaaggg	430		
PR	15-JUL-1999;	99US-0144005.	PR	07-OCT-1999;	99US-0158029.	Db	448	gcaactgaagcgggttatgtgaagcgaccgggaaggataaaagagataaccgaggcaaa	507		
PR	16-JUL-1999;	99US-0144085.	QY	08-OCT-1999;	99US-0158232.	QY	431	aagctagtggatgaggaagacattggtttctatcaaggctcgagctctcgagccgt	490		
PR	19-JUL-1999;	99US-0144325.	PR	12-OCT-1999;	99US-0158369.	PR	508	tcactgttggatgaagaagacactgttttctatagagggaagagctctctaaaggtcag	567		
PR	19-JUL-1999;	99US-0144331.	PR	13-OCT-1999;	99US-0159293.						
PR	19-JUL-1999;	99US-0144332.	PR	13-OCT-1999;	99US-0159294.						
PR	19-JUL-1999;	99US-0144333.	PR	13-OCT-1999;	99US-0159295.						
PR	19-JUL-1999;	99US-0144334.	PR	14-OCT-1999;	99US-0159329.						
PR	19-JUL-1999;	99US-0144335.	PR	14-OCT-1999;	99US-0159330.						
PR	20-JUL-1999;	99US-0144632.	PR	14-OCT-1999;	99US-0159637.						
PR	20-JUL-1999;	99US-0144632.	PR	14-OCT-1999;	99US-0159638.						
PR	21-JUL-1999;	99US-0144884.	PR	18-OCT-1999;	99US-0159584.						
PR	21-JUL-1999;	99US-0145114.	PR	21-OCT-1999;	99US-0160741.						
PR	21-JUL-1999;	99US-0145086.	PR	21-OCT-1999;	99US-0160767.						
PR	22-JUL-1999;	99US-0145085.	PR	21-OCT-1999;	99US-0160768.						
PR	22-JUL-1999;	99US-0145087.	PR	21-OCT-1999;	99US-0160770.						
PR	22-JUL-1999;	99US-0145089.	PR	21-OCT-1999;	99US-0160814.						
PR	22-JUL-1999;	99US-0145192.	PR	22-OCT-1999;	99US-0160815.						
PR	23-JUL-1999;	99US-0145145.	PR	22-OCT-1999;	99US-0160980.						
PR	23-JUL-1999;	99US-0145218.	PR	22-OCT-1999;	99US-0160981.						
PR	23-JUL-1999;	99US-0145224.	PR	22-OCT-1999;	99US-0160989.						
PR	26-JUL-1999;	99US-0145276.	PR	25-OCT-1999;	99US-0161404.						
PR	27-JUL-1999;	99US-0145913.	PR	25-OCT-1999;	99US-0161405.						
PR	27-JUL-1999;	99US-0145918.	PR	25-OCT-1999;	99US-0161406.						
PR	27-JUL-1999;	99US-0145919.	PR	26-OCT-1999;</							

Qy	491	aaacccgattgggtcatgcacgaatcccgctctccaaggatctcatcatctctcccaatcat	555
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Qy	551	tcctcgaagctctccaaaggaagactgggtctctgtgtagggtattccataagaatacggaa	610
Db	624	ttgccgaacccgcaagaagaatgaatgggtgatcgagggtgtccaaaagagtgctgga	683
Qy	611	gg 612	
Db	684	gg 685	
RESULT 14			
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ID	AAC39505 standard; DNA; 1368 BP.		
AC	AAC39505;		
XX			
DT	17-OCT-2000 (first entry)		
XX			
DE	Arabidopsis thaliana DNA fragment SEQ ID NO: 24879.		
XX			
KW	Hybridisation assay; genetic mapping; gene expression control;		
KW	protein identification; signal transduction pathway;		
KW	metabolic pathway; promoter; termination sequence; ss.		
XX			
OS	Arabidopsis thaliana.		
XX			
PN	EP1033405-A2.		
XX			
PD	06-SEP-2000.		
XX			
PF	25-FEB-2000; 2000EP-0301439.		
XX			
25-FEB-1999;	99US-0121825.		
05-MAR-1999;	99US-0123180.		
09-MAR-1999;	99US-0123348.		
23-MAR-1999;	99US-0125788.		
25-MAR-1999;	99US-0126264.		
29-MAR-1999;	99US-0126785.		
01-APR-1999;	99US-0127462.		
06-APR-1999;	99US-0128234.		
08-APR-1999;	99US-0128714.		
16-APR-1999;	99US-0129845.		
19-APR-1999;	99US-0130077.		
21-APR-1999;	99US-0130449.		
23-APR-1999;	99US-0130510.		
23-APR-1999;	99US-0130891.		
28-APR-1999;	99US-0131449.		
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30-APR-1999;	99US-0132407.		
04-MAY-1999;	99US-0132484.		
05-MAY-1999;	99US-0132485.		
06-MAY-1999;	99US-0132486.		
06-MAY-1999;	99US-0132487.		
07-MAY-1999;	99US-0132863.		
11-MAY-1999;	99US-0134256.		
14-MAY-1999;	99US-0134218.		
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18-MAY-1999;	99US-0134768.		
19-MAY-1999;	99US-0134941.		
20-MAY-1999;	99US-0135124.		
21-MAY-1999;	99US-0135353.		
24-MAY-1999;	99US-0135629.		
25-MAY-1999;	99US-0136021.		
27-MAY-1999;	99US-0136392.		
28-MAY-1999;	99US-0136782.		
01-JUN-1999;	99US-0137222.		
03-JUN-1999;	99US-0137528.		
04-JUN-1999;	99US-0137502.		

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PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 22-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161921.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match          12.4%; Score 159.8; DB 21; Length 1368;
Best Local Similarity 62.4%; Pred. No. 1.5e-34;
Matches 319; Conservative 0; Mismatches 182; Indels 10; Gaps 4;

QY 98 gaagaagagatgaagaaagtagtataagcatggtggaggcaaaagttgctccgggattc 157
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DB 110 gaagaaggtgtgtgttaaatcatggagtgaaagctgttgatttgcacctgggttc 169
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QY 158 agatttcaccggaagacgagcttctcgcgattacttgatgagacgatcgcttcac 217
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DB 170 aggtttcacaacagacagagatcataacatgttacccttaag---gagaaggtttta 226
   ||||| || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 218 aataatcatcgaccacctcttctcctgatccaagtcgatctcaacaagtgtgacctgg 277
   || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 227 aacagccgattcacggtgtgcccattggagagctgatctcaacaagtgtgacctgg 286
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QY 278 gacatcccaaaaatggcatgctggagggaagagattgttatttctacagccaagagac 337
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DB 287 gattggcc-aatagggcaaaagatggggagaaagattctactctctctgtcaaggagac 345
   || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 338 cgaaaatacgcgacgggctgagaactaacgcgacgcaacgcgcgcgcgcgcgcgcgcgc 397
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DB 346 aggaagatccgactgggatgagacgaaccgtgcgacggagtcaggatctggaagacc 405
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QY 398 accggcaaaagacagaccattcttaaga---aagggttaagctagttggatgaggaagaca 454
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DB 406 accgggaagataagagatcttcaaaaggcaaaaggttctcgttggatgaagaaaca 465
   ||||| || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 455 ttggtttctatcaaggtcgcgctcctcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 514
   || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 466 ctgtgttttatagaggagagctccaaaaggtgaaagagctaatgttggttcacatgaa 525
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QY 515 ttccgtctccaagatctcatctccctcccaatctctcgtcgcgcgcgcgcgcgcgcgcgc 574
   ||||| ||||| || | | | | | | | | | | | | | | | | | | | | | | | | |
DB 526 tatcgtcttgaaggcaaatattctattacaatc---tcccaaaatctgcaaggagacaa 582
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QY 575 tgggtctgtgttaggttattccataagaata 605
   ||||| ||||| || | | | | | | | | | | | | | | | | | | | | | | | | |
DB 583 tgggtcgtgttaggtttttccacaagaaca 613
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RESULT 15
AAD06464
ID AAD06464 standard; cDNA; 1479 BP.
XX AC AAD06464;
XX AC AAD06464;
DT 10-AUG-2001 (first entry)
DE Arabidopsis thaliana transcription factor G526 homologue, G765 cDNA.
KW Transcription factor; environmental stress tolerance; gene therapy;
  plant structure; plant development; ss.
XX Arabidopsis thaliana.
FH Key Location/Qualifiers
CDS 192..962
   /*tag= a
   /product= "Arabidopsis thaliana transcription factor
   homologue"
XX WO200136598-A1.
XX XX
XX 25-MAY-2001.
XX XX
XX 14-NOV-2000; 2000WO-US31458.
XX XX
PR 17-NOV-1999; 99US-0166228.
PR 17-APR-2000; 2000US-0197899.
PR 22-AUG-2000; 2000US-0227439.
XX XX
PA (MEND-) MENDEL BIOTECHNOLOGY INC.
PA (FINE/) PINEDA O.
PA (YUGG/) YU G.
PA (CREE/) CREELMAN R.

```



6

---















; INFORMATION FOR SEQ ID NO: 71:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1474 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-975-316-71

Query Match 2.8%; Score 36.6; DB 2; Length 1474;  
Best Local Similarity 76.3%; Pred. No. 0.24; Mismatches 0; Gaps 0;

QY 1219 ataccatcatgctagctagcttgcattgtttcaaaaaaaaaaaaaaaaaaaaaa 1277  
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Db 1397 AAATTAATATGATCTGCTATTATGAAAAAATAAAAAAAAAAAAAAAAAAAAA 1455

## RESULT 13

US-09-385-982-376  
; Sequence 376, Application US/09385982  
; Patent No. 6262334

; GENERAL INFORMATION:  
; APPLICANT: ENDEGE, WILSON O., ET AL.  
; TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION  
; FILE REFERENCE: CCNA-260XX  
; CURRENT APPLICATION NUMBER: US/09/385,982  
; CURRENT FILING DATE: 1999-08-30  
; EARLIER APPLICATION NUMBER: 09/328,111  
; EARLIER FILING DATE: 1999-06-08  
; EARLIER APPLICATION NUMBER: 60/117,393  
; EARLIER FILING DATE: 1999-01-27  
; EARLIER APPLICATION NUMBER: 60/098,639  
; EARLIER FILING DATE: 1998-08-31  
; NUMBER OF SEQ ID NOS: 544  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 376  
; LENGTH: 611  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(611)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-385-982-376

Query Match 2.8%; Score 36.4; DB 4; Length 611;  
Best Local Similarity 66.7%; Pred. No. 0.17; Mismatches 26; Indels 0; Gaps 0;

QY 1200 ataccacttgcgcgtagacacacatatatttcctgcgtgcttgcattgtttcaaaaaa 1259  
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Db 197 atgcgccttaccacgcgtactctactctctctctctctctctctctctctctctctctct 256

QY 1260 aaaaaaaaaaaaaaaaaa 1277  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 257 aaaaaaaaaaaaaaaaaa 274

## RESULT 14

US-08-226-264-27  
; Sequence 27, Application US/08226264  
; Patent No. 5801017

; GENERAL INFORMATION:  
; APPLICANT: Werber, Moshe M.  
; APPLICANT: Zeelon, Elisha P.  
; APPLICANT: Levanon, Avigdor  
; APPLICANT: Guy, Rachel  
; APPLICANT: Goldlust, Arie  
; APPLICANT: Rigbi, Meir  
; APPLICANT: Panet, Amos

; APPLICANT: Fischer, Meir  
; TITLE OF INVENTION: PRODUCTION OF RECOMBINANT FACTOR XA  
; INHIBITORS OF LEECH HIRUDO MEDICINALIS  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper & Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036  
; COMPUTER READABLE FORM: disk  
; MEDIUM TYPE: Floppy  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA: US/08/226,264  
; APPLICATION NUMBER: US/08/226,264  
; FILING DATE: 08-APR-94  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 40017-A/JPW/GJG  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-278-0400  
; TELEFAX: 212-391-0525  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 27:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 684 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
US-08-226-264-27

Query Match 2.7%; Score 35.2; DB 1; Length 684;  
Best Local Similarity 68.1%; Pred. No. 0.42; Mismatches 23; Indels 0; Gaps 0;

QY 1206 cttatgcgcgtagacacacatatatttcctgcgtgcttgcattgtttcaaaaaa 1265  
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Db 589 CTAATAATATGAAGATAAATATATATTTATCGTTCGCATATCAACATTCACAAAAA 648

QY 1266 aaaaaaaaaa 1277  
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Db 649 AAAAAAAAAA 660

## RESULT 15

US-09-232-200-36  
; Sequence 36, Application US/09232200A  
; Patent No. 6288213

; GENERAL INFORMATION:  
; APPLICANT: Stahl, Andreas  
; APPLICANT: Hirsch, David J.  
; APPLICANT: Lodish, Harvey F.  
; APPLICANT: Gimeno, Ruth E.  
; APPLICANT: Tartaglia, Louis A.  
; TITLE OF INVENTION: FATTY ACID TRANSPORT PROTEINS  
; FILE REFERENCE: WHI97-21p3MB  
; CURRENT APPLICATION NUMBER: US/09/232,200A  
; CURRENT FILING DATE: 1999-01-14  
; EARLIER APPLICATION NUMBER: 60/071,374  
; EARLIER FILING DATE: 1998-01-15  
; EARLIER APPLICATION NUMBER: 60/093,491  
; EARLIER FILING DATE: 1998-07-20  
; EARLIER APPLICATION NUMBER: 60/110,941  
; EARLIER FILING DATE: 1998-12-04

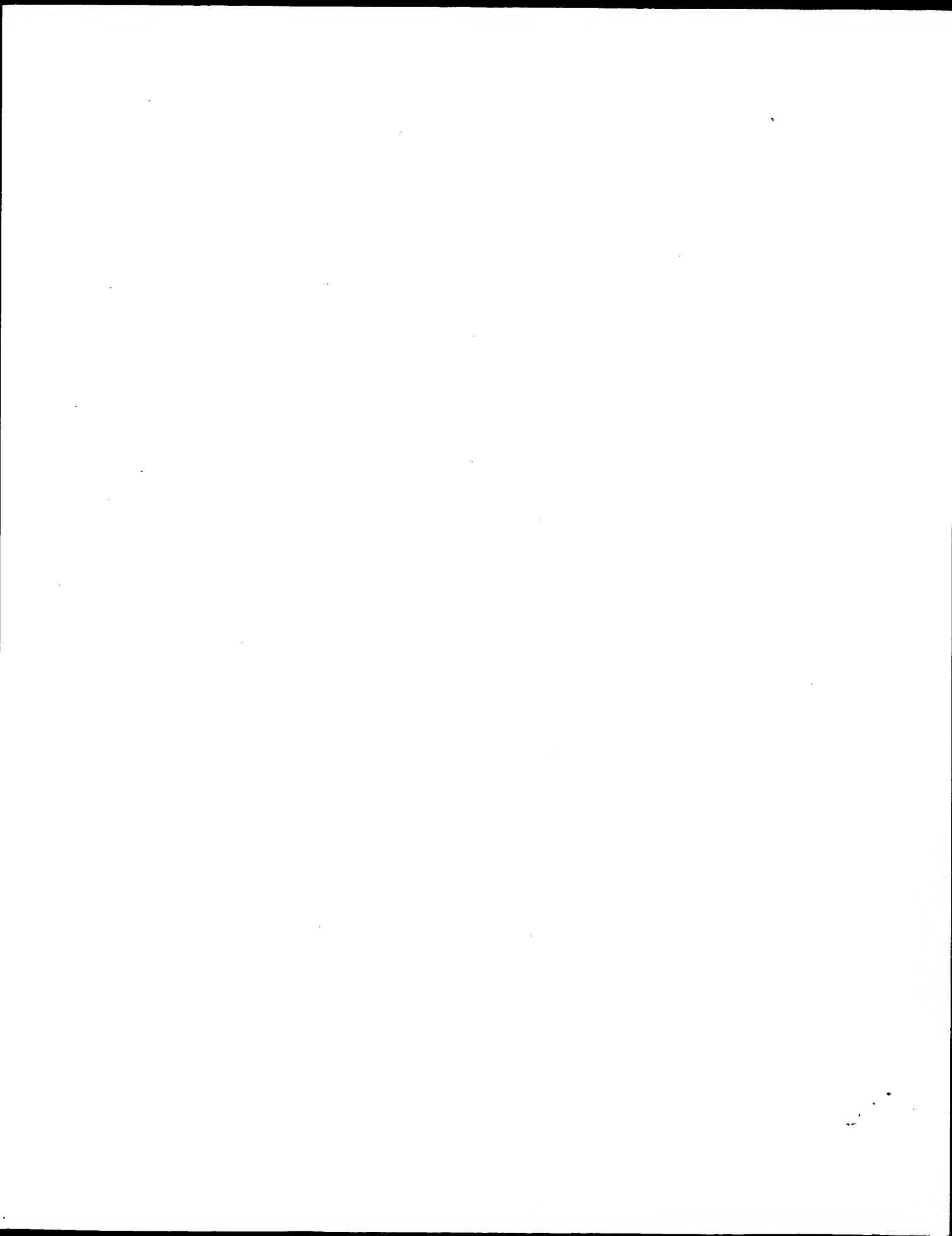
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; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 36
; LENGTH: 2885
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-232-200-36
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Query Match      2.7%; Score 35.2; DB 4; Length 2885;
Best Local Similarity 68.1%; Pred. No. 0.93;
Matches 49; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

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Db 2814 taaaatttctaatttgaataaaagattaaattttactgaaaaaaaaaaaaaaaaaa 2873

QY 1276 aaggcgccgcgc 1287
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Db 2874 attggcgccgc 2885
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Search completed: July 15, 2002, 07:09:09  
Job time: 1705 sec



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: July 15, 2002, 06:55:13 ; Search time 17.76 Seconds  
(without alignments)  
1752.981 Million cell updates/sec

Title: US-09-889-926-2

Perfect score: 1757

Sequence: 1 METEEMKRESSISMVEAKLP.....EGSSESLTLDIGIPSTVWNC 324

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Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR\_71.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	536.5	30.5	334	C96791	unknown protein Fl
3	505.5	28.8	316	E84636	NAM (no apical mer
4	491.5	28.0	365	G84559	probable NAM (no a
5	473	26.9	298	H96584	hypothetical prote
6	472.5	26.9	334	T47983	hypothetical prote
7	470.5	26.8	324	B96742	NAM-like protein, -
8	459.5	26.2	399	T02678	NAM (no apical mer
9	456	26.0	377	T04585	hypothetical prote
10	456	26.0	418	E86395	hypothetical prote
11	453.5	25.8	631	D96683	hypothetical prote
12	446.5	25.4	341	T04050	hypothetical prote
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15	436.5	24.8	317	B96570	NAM-like protein,
16	436	24.8	300	H96636	hypothetical prote
17	436	24.8	314	T09933	hypothetical prote
18	436	24.8	409	G86257	hypothetical prote
19	434	24.7	305	F86456	unknown protein [i
20	429	24.4	253	G96803	GRAB1-like protein
21	423.5	24.1	303	T52345	OSNAC6 protein [im
22	421	24.0	289	E86148	T1NG.12 protein -
23	420	23.9	329	T52344	-OSNAC5 protein [im
24	413.5	23.5	534	T04663	hypothetical prote
25	411	23.4	268	T52343	hypothetical prote
26	410.5	23.4	567	T48437	hypothetical prote
27	397.5	22.6	275	G84860	NAM (no apical mer
28	395	22.5	262	T05084	hypothetical prote
29	390.5	22.2	268	A84746	probable NAM (no a

30	378.5	21.5	315	2	T04624	hypothetical prote
31	374	21.3	283	2	F96450	hypothetical prote
32	370	21.1	272	2	T07182	hypothetical prote
33	366	20.8	276	2	D84547	NAM (no apical mer
34	363	20.7	176	2	G84436	NAM (no apical mer
35	362	20.6	335	2	C84671	NAM (no apical mer
36	361.5	20.6	557	2	B86466	hypothetical prote
37	358.5	20.4	576	2	A86466	BNF3b factor prote
38	347.5	19.8	469	2	T46230	NAC2-like protein
39	336	19.1	335	2	T49145	hypothetical prote
40	326	18.6	522	2	E86453	CDS protein F9L11.
41	309	17.6	220	2	T52100	ATAF2 protein - Ar
42	292.5	16.6	229	2	T52342	NAC-domain protein
43	283.5	16.1	229	2	S37101	ATAF1 protein - Ar
44	273.5	15.6	457	2	B85020	probable NAM-like
45	255	14.5	302	2	T01942	hypothetical prote

#### ALIGNMENTS

RESULT 1

C96601

hypothetical protein T6H22.19 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Mar-2001

C:Accession: C96601

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,

ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719

A:Accession: C96601

A>Status: Preliminary

A:Molecule type: DNA

A:Residues: 1-309 <STO>

A:Cross-references: GB:AB005173; NID:96056383; PIDN:AAF02847.1; GSPDB:GN00141

C:Genetics:

A:Gene: T6H22.19

A:Map position: 1

Query Match 89.9%; Score 1579.5; DB 2; Length 309;  
Best Local Similarity 91.8%; Pred. No. 1.9e-129;  
Matches 302; Conservative 0; Mismatches 2; Indels 25; Gaps 3;

QY 1 METEEMKRESSISMVEAKLPQGFPHPKDDELVC DYLMRRSLHNNHRRPPLVLIQVDLNKC 60

|||||

Db 1 METEEMKRESSISMVEAKLPQGFPHPKDDELVC DYLMRRSLHNNHRRPPLVLIQVDLNKC 60

|||||

QY 61 EPWDIP----KMACVGKDWYFYSDRDKVATGRTATATGYKATGDKRTTLRK GK 115

|||||

Db 61 EPWDIPMNTTKRVC-----QDRKATGRTATATGYKATGDKRTTLRK GK 111

|||||

QY 116 LVGMKRLTVFYOGRAPRGKTDVVMHFRLOQSHPPNHSLSPPKEDVWLRFVFKNTEG 175

|||||

Db 112 LVGMKRLTVFYOGRAPRGKTDVVMHFRLOQSHPPNHSLSPPKEDVWLRFVFKNTEG 160

|||||

QY 176 VTCRNMGSCFDETSASLPPLMDPYINFDQEPSSYLSDDHHYIINEHVPCFNSLNQQT 235

|||||

Db 161 VICRNMGSCFDETSASLPPLMDPYINFDQEPSSYLSDDHHYIINEHVPCFNSLNQQT 220

|||||

QY 236 LNSNLTNSVSELKIPCKNPPLFTGGSASATLTGLDSCSSDQWVLRALLSQLKIDGSL 295

|||||

Db 221 LNSNLTNSVSELKIPCKNPPLFTGGSASATLTGLDSCSSDQWVLRALLSQLKIDGSL 280

|||||

QY 296 GPKESQSYGEGSSESLTLDIGIPSTVWNC 324





Db 123 PNGKSDWIMHEVRLESDENAP-----PQEGWVVCRAFFKKRATGOAKNTWSSSYEV 176  
QY 187 DETASASLPPLMDPYINFDQEPSSYLSDHHYLIINEHVPCFNSLNSQNTLNSLTNSVSE 246  
Db 177 DEVAPNGVNSVMDPI-----DYISKOQHNIFGRGLMKQBEL-EGMVDGINYIQSNQF 227  
QY 247 LKIP-CKNPN-PLFTGGSASATLTGLDS 272  
Db 228 IQLPOLQSPSLPLMKRPSMSITSMDN 255

RESULT 5  
H96584  
hypothetical protein F20D21.15 [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Mar-2001  
C:Accession: H96584  
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,  
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Huizar, L.; Dewar, K.;  
ansen, N.F.; Hughes, B.; Huizar, L.  
Nature 408, 816-820, 2000  
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.  
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziali,  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,  
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A:Reference number: A86141; MUID:21016719  
A:Accession: H96584  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-298 <STO>  
A:Cross-references: GB:AE005173; NID:g4585977; PIDN:AA025613.1; GSPDB:GN00141  
C:Genetics:  
A:Gene: F20D21.15  
A:Map position: 1

Query Match 26.9%; Score 473; DB 2; Length 298;  
Best Local Similarity 40.1%; Pred. No. 2.2e-33;  
Matches 112; Conservative 26; Mismatches 61; Indels 80; Gaps 10;

QY 19 LPFGFRHPKDDDELVDYLMRRSLNHRPPLVLI-QVDLNKCEPMDIPKMACVCGK-- 75  
Db 3 LPFGFRHPDDELVAYLDKVV--NGQALELEIPEVDLYKCEPMDLPEKSFPLGNDME 60  
QY 76 WYFYSQDRKRYATGLTNRTATGYWKATGKORTILRKGLVGMKRTLVFYOGGRAPGRK 135  
Db 61 WYFYSTDKKYPNGSTNRATRAGYWKATGKORTVSKKMKMGKTKLVYRGRAPGLR 120  
QY 136 TDWVMEFRLOGSHHPNHSLSPPKEDWVLCRVFHN----- 172  
Db 121 TNWVMEYRUT---HAPSSSL---KESYALCRVFKKNIQIPKKGEEAEESTSVGKE 174  
QY 173 -----TEGVICRD-----NNGSCFDETSASLPPLMDPYINFDQ 206  
Db 175 EEEKEKKWKRCGNYIEDSLKRASETSSSELTQGVLLDEANSSI-----PAL 225  
QY 207 EPSYSLSDHHYIINE-----HVP-----FSNLSQNG 234  
Db 226 HFSSSLDDHDLFSNYSHQLPYHPPLQLQDFPLSMNE 264

RESULT 6  
T47983  
NAM-like protein - Arabidopsis thaliana  
N:Alternate names: protein F21F14.80  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 20-Apr-2000  
C:Accession: T47983  
R:Cholsne, N.; Robert, C.; Brottier, P.; Wincker, P.; Cattolico, L.; Artiguenave, F.; Sa  
submitted to the Protein Sequence Database, February 2000

A:Reference number: Z24481  
A:Accession: T47983  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-334 <CHO>  
A:Cross-references: EMBL:AL138642  
A:Experimental source: cultivar Columbia; BAC clone F21F14  
C:Genetics:  
A:Map position: 3  
A:Introns: 58/1  
A:Note: F21F14.80

Query Match 26.9%; Score 472.5; DB 2; Length 334;  
Best Local Similarity 33.1%; Pred. No. 2.8e-33;  
Matches 119; Conservative 52; Mismatches 89; Indels 99; Gaps 15;

QY 16 EAKLPPGFRHPKDDDELVDYLMRRSLNHRPPLVLIQVDLNKCEPMDIPKMACVCG--- 72  
Db 8 QSOVPPGFRHPTEELL-KYVLRKKISNIKIDLDVDPIDLNKLEPDIQEMCKIGTTP 66  
QY 73 GKDWTFYSQDRKRYATGLTNRTATGYWKATGKORTILRKGLVGMKRTLVFYOGGRAPR 132  
Db 67 QNDWTFYSKDKKYPGTGTRATRVGFWKATGTRDKTIYTNNGDRIGMRKTLVYFKGRAPH 126  
QY 133 GRKTDVWMEFRLO-----GSH--HPPNHSLSPPKEDWVLCRVFHNKTEGVICRDNM 182  
Db 127 GOKSDWIMHEFRVLDSEVLISCGDHDVNVETCDVIGSDGWWVVCVFKNN---LCKNMI 183  
QY 183 GS-----CFDETSASLPPLM-----DPYINFDQEPSSYLSLDDHHYIINEH 223  
Db 184 SSSPASSVVKTPFNEETIEQLLEVWGQSKGEIVLDPFLK-----PN 226  
QY 224 VPCFSN--LSQNTLNSLTNS--VSELKIPCKNPNPLFTGGSASATLTGLDSCSDQM 279  
Db 227 LECHNNTTITSYQWLIDDQVNVCHVSKYMDP-----SFTSWAA 265  
QY 280 VLRLALLSOLTKIDGSLGP-----KESQSVG---EGSSESLTLDIGIPS-TWYN 323  
Db 266 LDRIVASQLN-----GPNYSIIPAVNETSQSPHYGLNRSCTGLTPDYIPEIDLWN 318

RESULT 7  
B96742  
NAM-like protein, 48543-50167 [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Mar-2001  
C:Accession: B96742  
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon  
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Huizar, L.; Dewar,  
ansen, N.F.; Hughes, B.; Huizar, L.  
Nature 408, 816-820, 2000  
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,  
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marzia  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo  
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A:Reference number: A86141; MUID:21016719  
A:Accession: B96742  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-324 <STO>  
A:Cross-references: GB:AE005173; NID:g6978918; PIDN:AAF34310.1; GSPDB:GN00141  
C:Genetics:  
A:Gene: F17M19.8  
A:Map position: 1

Query Match 26.8%; Score 470.5; DB 2; Length 324;  
Best Local Similarity 35.1%; Pred. No. 4e-33;  
Matches 107; Conservative 52; Mismatches 75; Indels 71; Gaps 10;

Qy	13	SMWEAKLPPOGFRHPKDDDELVCVDLMRRSLHNNHRPPL-VLIQVDLNKECPWDIPKMCAV	71
		: : : : :           :       :   : : : :	:
Db	3	NIMQSSMPPGFRFPHTEELVGVLORKI - NSMKSA LDVIWEIDLXKMEPWDIQARCKL	60
		: : : : :           :       :   : : : :	:
Qy	72	G---GKDWFYSQRDKYATGLTNRATATGWKATGDKDRTILRGKGLVGMKRTLIVFYQG	128
		: : : :           :       :   : : : :	:
Db	61	GYBEQNEWFFSHKDRKYPTGTTRNRTAAGFWKATGRDKAVLSKNSVTGMKRTLIVLYKG	120
		: : : : :           :       :   : : : :	:
Qy	129	RAPRGRKTDMWHEFRLOQSHHPHNISLASPREDDWLVCRFHKNTEGVICRDNMGCDFE	188
		:           :       :   : : : :	:
Db	121	RAPNGRKSDWIHHEYLRQNSELAP-----VQEEGWVVCRAFRK-----	158
		: : : : :           :       :   : : : :	:
Qy	189	TASASLIPPLMDPVINFDOEPSSVLSDDHYIINEHVPCFSNLSONOTLN-----SNLT	241
		: : : : :           :       :   : : : :	:
Db	159	----PIP-----NQRLGVEPNQOLY---HVESSNNVTSSSVMTNTSHHCASSSS	202
		: : : : :           :       :   : : : :	:
Qy	242	NSVSELIKPCKNPNPLFTGGS-----ASATITGLIDSPCSDQMWLRALLSQLTKDGSLG	297
		: : : : :           :       :   : : : :	:
Db	203	HNLNQMLMSNNHYNPNNTSSSHOYGNIELPOLDS-----PSLSPSLGT	246
		: : : : :           :       :   : : : :	:
Qy	298	KESOS	302
		: : : : :	:
Db	247	NKDON	251
		: : : : :	:

RESULT 8

T02678  
NAM (no apical meristem)-like protein [imported] - Arabidopsis thaliana  
N:Alternate names: hypothetical protein F19D11.5  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C>Date: 24-Mar-1999 #sequence\_revision 24-Mar-1999 #text\_change 02-Feb-2001  
C:Accession: T02678 #A84907  
R:Rounsley, S.D.; Lin, X.; Kaul, S.; Shea, T.P.; Fujii, C.Y.; Shen, M.; Ron  
submitted to the EMBL Data Library, September 1998  
A:Description: Arabidopsis thaliana chromosome II BAC F19D11 genomic sequence.  
A:Reference number: Z14698  
A:Accession: T02678  
A>Status: translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-399 <ROU>  
A:Cross-references: EMBL:AC005310; NID:g3510247; PID:g3510262  
A:Experimental source: cultivar Columbia  
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;  
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, J.  
nature, D.; Nierman, W.C.; White, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.  
Oxford 402, 761-768, 1999  
A>Title: Sequence and analysis of chromosome 2 cf the plant Arabidopsis thaliana.  
A:Reference number: A84420; MUID:20083487  
A:Accession: A84907  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-399 <SFO>  
A:Cross-references: GB:AE002093; NID:g3510262; FIDN:AAC33506.1; GSPDB:GN00139  
C:Genetics:  
A:Gene: At2g46770; F19D11.5  
A:Map position: 2  
A:Introns: 62/1; 157/3; 362/1

	Query Match	26.2%	Score 459.5;	DB 2;	Length 399;
	Best Local Similarity	32.2%;	Pred. No. 4.8e-32;		
	Matches 119; Conservative	65;	Mismatches 103;	Indels 83;	Gaps 17;
Qy	8 KESSISM-VEAKLPFGFRHFKDDELVC DYLMRRSLHNHNRPPLVLIQVDLNKCEPDWIP	66			
	: : : :           :   : : :				
Db	3 KMSISVNGSQSVPGPGRFHFEELL-QYYLRKKVNSEIEDLDVIDRDVLNKLPEWDIQ	61			
Qy	67 KMACVG---GKDWFYSQRDRKYATGLTNRATATGYWKATGKTORTILRKGKLVGMRTL	123			
	:				
Db	* 62 EMCKIGITPQNDWYFFSHKDKKYPTGTNRATAAGFWKATGROKI IYSNGRRIGMRTL	121			
	:				
Qy	124 VFYQGRAPRGKRTDWVMHEFLRQLQSGHHPPN-----HSL-----SSPKEDWVLCRVF--	170			

```

Db      122 VFYGRAPHGQKDWIMHETRLDNIISPEDVTVHEVVSIIGEASQDEGWVVCRIFFKKK 181
Qy      171 -----KNTGVICRDN-----MG-SCFDEITASLPLMDP 200
Db      182 LHKTLNPSVGCASLGGGDPKTTSSQIFNEDTLDQFELMGRSCKEELN-----LDP 234
Qy      201 YINFD--QEPSSYLSDDHHYIINHVV---PCFSNLSONQTLNSLNTSVSEL-KIPCKNP 254
Db      235 FMKLPNLESPPNS-----QAINNCHVSSPDFTNHHVSNVVDTSFVTSWAAALDLVASQL 288
Qy      255 NPLFTGGSASATLTCL-DSPCSSDQMLRALLSQTLDGSLGPKESQSYGEGSSESLTT 313
Db      289 N-----GFTSYISITAVNESHVGHDLALPSVRSYPYSLN-----RSASYHAGLTQEYTP 337
Qy      314 DIGIPSTVWN 323
Db      338 EM----ELWN 343

RESULT 9
T04585
hypothetical protein F23E13.50 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 14-May-1999
C:Accession: T04585
R:Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Jesse,
submitted to the Protein Sequence Database, March 1998
A:Reference number: Z15378
A:Accession: T04585
A:Molecule type: DNA
A:Residues: 1-377 <BEV>
A:Cross-references: EMBL:AL022141
A:Experimental source: cultivar Columbia; BAC clone F23E13
C:Genetics:
A:Map position: 4
A:Introns: 57/1; 147/3
A:Note: F23E13.50

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Query Match	26.0%;	Score 456;	DB 2;	Length 377;	
Best Local Similarity	32.3%;	Pred. No. 8.9e-32;			
Matches	120;	Conservative 56;	Mismatches 91;	Indels 104;	Gaps 16;
Qy	19	LPPGFRHPKDELVCVDYLMRRSLNNHRPPLVLIVQDLNKCPEWDIPKMACVG--GKD	75		
Db	10	VPPGFRFHTDEELV-GYYLRKKVASQKIDLDVINDIDLYRIEPWDLOESCRIGVEERNE	68		
Qy	76	WYFYSQRDRKATGLRTNRATATGYWKATGDKDRTILRRKGLVGMKRTILVYQGRAPGRK	135		
Db	69	WYFESHKDKPYTGTRTNATMAGFWKATGRDKAVYDKSKLIGMRKTLVLYFKGRAPNGOK	128		
Qy	136	TDWVNHFRLOGSHHPPNHSLSSPKED-WVLCRVFH-----KNTBGVTCIRDNMGSCF	186		
Db	129	TDWIMHEYRLSDENAP-----PQEEGVVYCFRAFKKKPMTGQAKNTE-----TWSSSYFY	178		
Qy	187	DETASASLPPLMDPVINFDPSPSYLSDDDHYIINE-----HVPQCFs	228		
Db	179	DELPSG-----VRSVTPELVNVSKQKONVFAQDLMFKQLEGSDIGLNFHCDQFI	229		
Qy	229	NLSNQTLNSNLT-----NSVSELKIPCKNP-----NPLFTGGS-----	262		
Db	230	QLPOLSESPSLTKRPVSLTSTSLE---KNKNITYKRHLIEEDVSFNALISSGNKDKKKK	286		
Qy	263	ASAVLT-----GLDSFCSDDQWVLRAALLSOLTKIDGSLG-----PKESQSYG-	304		
Db	287	KTSVMTTDDWRALDKFVASQ-----LMSQDGVSGFGGHHEDNNKIGHYANNEESNNKGS	340		
Qy	305	-EGSSESLLTD	314		
Db	341	VETASSTLLSD	351		
RESULT	10				



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Search completed: July 15, 2002, 06:57:27  
Job time: 134 sec



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: July 15, 2002, 06:56:48 ; Search time 13.42 Seconds  
(without alignments)  
934.809 Million cell updates/sec

Title: US-09-889-926-2

Perfect score: 1757

Sequence: 1 METEEMKRESSISMVEAKLP.....EGSSBSLLTDIGIPSTVWNC 324

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	106	6.0	1872	1 T2D1_HUMAN	P21675 homo sapien
2	95	5.4	3092	1 IRAL1_YEAST	P18963 saccharomyc
3	95	5.4	3969	1 HRX_HUMAN	Q03164 homo sapien
4	87.5	5.0	314	1 Y009_HUMAN	Q15390 homo sapien
5	87.5	5.0	928	1 PM11_CHLPN	O86164 chlamydia p
6	87.5	5.0	3866	1 HRX_MOUSE	P55200 mus musculu
7	86.5	4.9	1377	1 CID_DROME	P19538 drosophila
8	85	4.8	530	1 GP2_RAT	P19218 rattus norv
9	85	4.8	610	1 UVRC_ECOLI	P07028 escherichia
10	84.5	4.8	429	1 NPT1_YEAST	P39683 saccharomyc
11	84.5	4.8	1182	1 HAIR_MOUSE	O61645 mus musculu
12	84.5	4.8	1458	1 PA2R_RABIT	P49260 oryctolagus
13	83.5	4.8	337	1 YDTB_SCHPO	O14216 schizosacch
14	83.5	4.8	591	1 IF37_ARATH	P56820 arabidopsis
15	82.5	4.7	584	1 ENV_IPMAE	P31789 mouse intra
16	82	4.7	584	1 YBX1_SCHPO	Q10207 schizosacch
17	81.5	4.6	1181	1 HAIR_RAT	P97609 rattus norv
18	81.5	4.6	2222	1 CCAE_RAT	Q07652 rattus norv
19	81	4.6	271	1 VA04_VAPV	P33832 variola vir
20	81	4.6	3125	1 POLG_PPVNA	P17766 p genome po
21	80	4.6	368	1 VE2_HPVA5	P36794 human papil
22	80	4.6	894	1 FOX2_NEUCR	Q01373 neurospora
23	80	4.6	1142	1 MGCI_HUMAN	O60732 homo sapien
24	79.5	4.5	454	1 MUC_HUMAN	P01871 homo sapien
25	79.5	4.5	510	1 YD85_SCHPO	Q10410 schizosacch
26	79.5	4.5	765	1 AMDR_EMENI	P15699 emericeella
27	79.5	4.5	969	1 AGLU_SCHPO	Q9C0Y4 schizosacch
28	79.5	4.5	1117	1 YN96_YEAST	P53753 saccharomyc
29	79.5	4.5	1210	1 ICEN_PSEFL	P09815 pseudomonas
30	79	4.5	356	1 POU1_XENLA	P31363 xenopus lae
31	79	4.5	458	1 YW51_YEAST	P42933 saccharomyc
32	79	4.5	479	1 XYL4_HORVU	Q40082 hordeum vul
33	79	4.5	711	1 RED1_RAT	P51400 rattus norv

34 79 4.5 726 1 K182\_YEAST  
35 79 4.5 971 1 CLA4\_CANAL  
36 79 4.5 4655 1 LRP2\_HUMAN  
37 78.5 4.5 468 1 PCO1\_MOUSE  
38 78.5 4.5 478 1 ARDE\_CHLMU  
39 78.5 4.5 978 1 SIR3\_YEAST  
40 78.5 4.5 1468 1 N153\_RAT  
41 78 4.4 391 1 MUCB\_HUMAN  
42 78 4.4 837 1 STA6\_MOUSE  
43 78 4.4 2182 1 CAB1\_RAT  
44 77.5 4.4 181 1 BY55\_HUMAN  
45 77.5 4.4 590 1 YNW7\_YEAST

## ALIGNMENTS

RESULT 1  
T2D1\_HUMAN  
ID T2D1\_HUMAN STANDARD; PRT: 1872 AA.  
AC P21675;  
DT 01-MAY-1991 (Rel. 18, Created)  
DT 01-MAY-1992 (Rel. 22, Last sequence update)  
DT 15-JUL-1998 (Rel. 36, Last annotation update)  
DE Transcription initiation factor TFIID 250 kDa subunit (TAFII-250)  
DE (TAFII250) (TBP-associated factor 250 kDa) (P250) (Cell cycle gene 1 protein).  
DE  
GN TAF2A OR CCG1 OR BA2R.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Laryngeal carcinoma;  
RX MEDLINE=91246200; PubMed=2038334;  
RA Sekiguchi T., Nohiro Y., Nakamura Y., Hisamoto N., Nishimoto T.;  
RT "The human CCG1 gene, essential for progression of the G1 phase, encodes a 210-kilodalton nuclear DNA-binding protein.";  
RL Mol. Cell. Biol. 11:3317-3325(1991).  
RN [2]  
RP PRELIMINARY SEQUENCE FROM N.A.  
RX MEDLINE=89005056; PubMed=3169001;  
RA Sekiguchi T., Miyata T., Nishimoto T.;  
RT "Molecular cloning of the cDNA of human X chromosomal gene (CCG1) which complements the temperature-sensitive G1 mutants, tsBN462 and ts13, of the BHK cell line.";  
RL EMBO J. 7:1683-1687(1988).  
RN [3]  
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.  
RX MEDLINE=93196704; PubMed=7680771;  
RA Ruppert S., Wang E.H., Tjian R.;  
RT "Cloning and expression of human TAFII250: a TBP-associated factor implicated in cell-cycle regulation.";  
RL Nature 362:175-179(1993).  
RN [4]  
RP CHARACTERIZATION.  
RX MEDLINE=93196705; PubMed=8450888;  
RA Hisatake K., Hasegawa S., Takada R., Nakatani Y., Horikoshi M., Roeder R.G.;  
RT "The P.50 subunit of native TATA box-binding factor TFIID is the cell-cycle regulatory protein CCG1.";  
RL Nature 362:179-181(1993).  
CC -!- FUNCTION: MAY PLAY AN ESSENTIAL ROLE IN TFIID ASSEMBLY BY INTERACTING WITH BOTH TBP AND OTHER TAF, AS WELL AS SERVING TO LINK THE CONTROL OF TRANSCRIPTION TO THE CELL CYCLE. ESSENTIAL FOR PROGRESSION OF THE G1 PHASE OF THE CELL CYCLE. POSSESSES DNA-BINDING ACTIVITY.  
CC -!- SUBUNIT: TFIID IS COMPOSED OF TBP AND A VARIETY OF TBP-ASSOCIATED FACTORS.  
CC -!- SUBCELLULAR LOCATION: Nuclear.  
CC -!- PTM: PHOSPHORYLATED BY CASEIN KINASE II IN VITRO.  
CC -!- SIMILARITY: CONTAINS 2 BROMODOMAINS.

P25341 saccharomyc  
O14427 candida alb  
P98164 homo sapien  
Q61398 mus musculu  
P56961 chlamydia m  
P06701 saccharomyc  
P49791 rattus norv  
P04220 homo sapien  
P52633 mus musculu  
O88480 rattus norv  
O95971 homo sapien  
P53863 saccharomyc







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```
CC CC CC CC CC
DR EMBL; L04284; AAS58669.1; -
DR EMBL; 269744; CAA93625.1; -
DR EMBL; 269745; CAA93625.1; JOINED.
DR EMBL; 269746; CAA93625.1; JOINED.
DR EMBL; 269747; CAA93625.1; JOINED.
DR EMBL; 269748; CAA93625.1; JOINED.
DR EMBL; 269749; CAA93625.1; JOINED.
DR EMBL; 269750; CAA93625.1; JOINED.
DR EMBL; 269751; CAA93625.1; JOINED.
DR EMBL; 269752; CAA93625.1; JOINED.
DR EMBL; 269753; CAA93625.1; JOINED.
DR EMBL; 269754; CAA93625.1; JOINED.
DR EMBL; 269755; CAA93625.1; JOINED.
DR EMBL; 269756; CAA93625.1; JOINED.
DR EMBL; 269757; CAA93625.1; JOINED.
DR EMBL; 269758; CAA93625.1; JOINED.
DR EMBL; 269759; CAA93625.1; JOINED.
DR EMBL; 269760; CAA93625.1; JOINED.
DR EMBL; 269761; CAA93625.1; JOINED.
DR EMBL; 269762; CAA93625.1; JOINED.
DR EMBL; 269763; CAA93625.1; JOINED.
DR EMBL; 269764; CAA93625.1; JOINED.
DR EMBL; 269765; CAA93625.1; JOINED.
DR EMBL; 269766; CAA93625.1; JOINED.
DR EMBL; 269767; CAA93625.1; JOINED.
DR EMBL; 269768; CAA93625.1; JOINED.
DR EMBL; 269769; CAA93625.1; JOINED.
DR EMBL; 269770; CAA93625.1; JOINED.
DR EMBL; 269772; CAA93625.1; JOINED.
DR EMBL; 269773; CAA93625.1; JOINED.
DR EMBL; 269774; CAA93625.1; JOINED.
DR EMBL; 269775; CAA93625.1; JOINED.
DR EMBL; 269776; CAA93625.1; JOINED.
DR EMBL; 269777; CAA93625.1; JOINED.
DR EMBL; 269778; CAA93625.1; JOINED.
DR EMBL; 269779; CAA93625.1; JOINED.
DR EMBL; 269780; CAA93625.1; JOINED.
DR EMBL; D14540; BAA03407.1; -
DR EMBL; L01986; AAA92511.1; -
DR EMBL; U04737; AAA18644.1; -
DR EMBL; S78570; AAB34770.1; -
DR EMBL; X81604; CAA58584.1; -
DR EMBL; S66432; AAB28545.1; -
DR EMBL; AF231998; AAG26332.2; ALT_TERM.
DR TRANSFAC; T02337; -
DR MIM; 159555; -
DR InterPro; IPR001487; Bromodomain.
DR InterPro; IPR003889; FYrich_C.
DR InterPro; IPR003888; FYrich_N.
DR InterPro; IPR001965; PHD.
DR InterPro; IPR003616; PostSET.
DR InterPro; IPR001214; SET.
DR InterPro; IPR002857; Znf-CXXC.
DR Pfam; PF00628; PHD; 3.
DR Pfam; PF00856; SET; 1.
DR Pfam; PF02008; zf-CXXC; 1.
DR SMART; SM00297; BROMO; 1.
DR SMART; SM00542; FYRIC; 1.
DR SMART; SM00541; FYRN; 1.
DR SMART; SM00249; PHD; 4.
DR SMART; SM00508; PostSET; 1.
DR SMART; SM00317; SET; 1.
DR PROSITE; PS00014; BROMODOMAIN_2; 1.
DR PROSITE; PS0280; SET; 1.
KW Proto-oncogene; Chromosomal translocation; DNA-binding; Bromodomain;
KW Nuclear protein; Zinc-finger; Metal-binding; Transcription regulation;
KW Alternative splicing.
```

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FT DOMAIN 17 102 ALA/GLY/SER-RICH.
FT DNA_BIND 169 180 A.T HOOK (BY SIMILARITY).
FT DNA_BIND 217 227 A.T HOOK (BY SIMILARITY).
FT DNA_BIND 301 309 A.T HOOK (BY SIMILARITY).
FT ZN_FING 1147 1194 CXXC-TYPE.
FT ZN_FING 1431 1482 PHD-TYPE 1.
FT ZN_FING 1484 1533 PHD-TYPE 2.
FT ZN_FING 1566 1627 PHD-TYPE 3.
FT DOMAIN 1703 1748 BROMODOMAIN (DIVERGENT).
FT DOMAIN 137 143 SET.
FT DOMAIN 561 564 POLY-GLY.
FT DOMAIN 568 571 POLY-PRO.
FT SITE 1362 1363 BREAKPOINT FOR TRANSLOCATION TO FORM MLL-

Query Match 5.4%; Score 95; DB 1; Length 3969;
Best Local Similarity 21.1%; Pred. No. 10;
Matches 68; Conservative 39; Mismatches 124; Indels 92; Gaps 13;

QY 38 MRRSLHNNRPPLVLIQV-----DLNKEPMDIPKMACYGGKDWYFYSDRDK 85
Db 2006 LRRKFLNGLEPENIHMMIGSMTIDCLGILNLDSDCE-----DKL 2044

QY 86 YATGLTNRATATGYWKATGKDRILRKGLVGRKTLVFGYGRAPRKRTDWMHEFRL 145
Db 2045 FPIGYQCSRV-----YWTTDARKRCVYTKIVECRPPV-----EPDINST--VEHDENR 2093

QY 146 QGSHHPNHSLSPEKEDWVLCRVFHNKTEGVC-----RDNMGSCDEFATASLPP 196
Db 2094 TIAHSPTSFTESSSKES-----QNTAEIISPPSDRPPHSGTSGCYHYHVIS-KVPR 2144

QY 197 LMDP-YINFDOEP-----SSYLSDDHHVILNEHVPCFNSLQNTLNSLNTNSYSELK 248
Db 2145 IRTEYSYPTQRSGCRLPAGSPTTTHIVTVGDPLLSGLRSIGRRHRHSSSSLPQR 2204

QY 249 IPCKNPPLFTGG-----SASATLGLDSFCSSDQWVLRAL-----LSQLTKIDG 293
Db 2205 SKLIMSPMRGTNTYRNNTYSSVSTTGTATDLESSAKVVDHVLGPLNSSLQNTSTSS 2264

QY 294 SL-----GPKESQSYGESSE 309
Db 2265 NLQRTVTVTVGNKSHLDGSSSE 2287

RESULT 4
Y009_HUMAN STANDARD; PRT; 314 AA.
ID Y009_HUMAN
AC Q15390;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein KIAA0009.
GN KIAA0009.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Bone marrow;
RX MEDLINE=96051387; PubMed=7584026;
RA Nomura N., Miyajima N., Suzuki T., Tanaka A., Kawarabayashi Y.,
RA Sato S., Nagase T., Seki N., Ishikawa K.-I., Tabata S.
RT "Prediction of the coding sequences of unidentified human genes. I.
RT The coding sequences of 40 new genes (K1A0001-K1A0040) deduced by
RT analysis of randomly sampled cDNA clones from human immature myeloid
RT cell line KG-1."
RL DNA Res. 1:27-35(1994).
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## RESULT 6

HRX\_MOUSE STANDARD; PRT; 3866 AA.

AC P55200;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 01-MAR-2002 (Rel. 41, Last annotation update)

DE Zinc finger protein HRX (ALL-1) (Fragment).

GN MLL OR HRX OR ALL1.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).

RC STRAIN=C57BL/6J, AND B6/CBA; TISSUE=Spleen, and Lung;

RA MEDLINE=93317679; PubMed=8327517;

RA Ma Q., Alder H., Nelson K.K., Chatterjee D., Gu Y., Nakamura T.,

RA Canaani E., Croce C.M., Siracusa L.D., Buchberg A.M.;

RT "Analysis of the murine All-1 gene reveals conserved domains with

RT human ALL-1 and identifies a motif shared with DNA

RT methyltransferases.";

RL Proc. Natl. Acad. Sci. U.S.A. 90:6350-6354(1993).

CC -!- FUNCTION: POSSIBLY ACTS AS A TRANSCRIPTIONAL REGULATORY FACTOR.

CC MAY REGULATE GENES INVOLVED IN SKELETAL FORMATION DURING

CC EMBRYONIC DEVELOPMENT.

CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).

CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2; ARE

CC PRODUCED BY ALTERNATIVE SPLICING.

CC -!- SIMILARITY: BELONGS TO THE TRANSCRIPTION FACTOR TRITHORAX FAMILY.

CC -!- SIMILARITY: CONTAINS 1 BROMODOMAIN.

CC -!- SIMILARITY: CONTAINS 1 SET DOMAIN.

CC -!- SIMILARITY: CONTAINS 3 PHD-TYPE ZINC FINGERS.

CC -!- SIMILARITY: CONTAINS 1 CXXC-TYPE ZINC FINGER.

CC -----

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CC -----

DR EMBL; LI7069; AAA62593.1; -

DR MGD; MGI:96995; M1.

DR InterPro: IPR001487; Bromodomain.

DR InterPro: IPR003889; FYrich\_C.

DR InterPro: IPR003888; FYrich\_N.

DR InterPro: IPR001965; PHD.

DR InterPro: IPR003616; PostSET.

DR InterPro: IPR000093; RecF.

DR InterPro: IPR001214; SET.

DR InterPro: IPR002857; znf-CXXC.

DR Pfam; PF00628; PHD; 3.

DR Pfam; PF00856; SET; 1.

DR SMART; SM00297; BROMO; 1.

DR SMART; SM00542; FYRC; 1.

DR SMART; SM00541; FYRN; 1.

DR SMART; SM00249; PHD; 4.

DR SMART; SM00508; PostSET; 1.

DR SMART; SM00317; SET; 1.

DR PROSITE; PS50014; BROMODOMAIN\_2; 1.

DR PROSITE; PS50280; SET; 1.

KW DNA-binding; Nuclear protein; Zinc-finger; Metal-binding;

KW Transcription regulation; Alternative splicing; Polymorphism.

FT NON\_TER 1 1

FT DNA\_BIND 67 78 A-T HOOK (BY SIMILARITY).

FT DNA\_BIND 115 125 A-T HOOK (BY SIMILARITY).

FT DNA\_BIND 199 207 A-T HOOK (BY SIMILARITY).

FT ZN\_FING 1044 1091 CXXC-TYPE.

FT ZN\_FING 1330 1381 PHD-TYPE 1.

FT ZN\_FING 1383 1432 PHD-TYPE 2.

FT ZN\_FING 1465 1529 PHD-TYPE 3.

FT DOMAIN 1605 1650 BROMODOMAIN (DIVERGENT).

FT DOMAIN 3737 3846 SET.

FT DOMAIN 35 41 POLY-GLY.

FT DOMAIN 459 469 PRO-RICH.

FT DOMAIN 1231 1238 POLY-PRO.

FT DOMAIN 3533 3536 POLY-GLU.

FT DOMAIN 3693 3697 POLY-GLU.

FT VARSPIC 1503 1505 MISSING (IN ISOFORM 2).

FT VARIANT 1497 1497 K -> T.

SO SEQUENCE 3866 AA; 420976 MW; ADFC55E14E806FID CRC64;

Query Match 5.0%; Score 87.5; DB 1; Length 3866;

Best Local Similarity 19.5%; Pred. No. 46;

Matches 63; Conservative 43; Mismatches 140; Indels 77; Gaps 11;

QY 38 MRRSLNHRPLVLIQV-----DLNKEPWPDPKMACVGGKDWYFYSDRDK 85

DB 1908 LRRKFLGLEPENTHMMIGMTIDCLGLNLSDC-----DKL 1946

QY 86 YATGLTNRATATGYKATGKDRILRKGLVGRKTLVFYQGRAPRKTDWVWHEFRL 145

DB 1947 FPIGQCSRV---YWSTTDARKRCVYTKIMECPVW-----EPDINST--VEHDDNR 1995

QY 146 QGSHPPNHSLSPEKDWVLCRVF-----HKNTGEVICRDMNGSCFDETSASLPL 197

DB 1996 TIAHSPSFIDASCCKDSQSTAAILSPSPDRPHSOTS-----GSCYHVVIS-KVPRI 2046

QY 198 MDP-YINFDEP-----SSYLSDDHHYIINEHVPCFNSLSONQTLNSLTSVSELKI 249

DB 2047 RTPSYSPQTSRPGCRPLPSAGSPPTTHEIVTGDPLLSGLRSIGRRHSTSLSPRS 2106

QY 250 PCKNPPLFTGGASATL-----TGLDSFCSDDQVLFALLSQTLDGSLGPKESQ 301

DB 2107 KLRIMSPVTSAYSRSSVSPSLGTATDEASAKADRGGLSSANLGHSAAPPSSS 2166

QY 302 SYGEGSSSLTLDIGIPSTVWNC 324

DB 2167 QRTVGGSKTSHLDGSSPSEVKRC 2189

RESULT 7

CID\_DROME ID CID\_DROME STANDARD; PRT; 1377 AA.

AC P19538;

DT 01-NOV-1990 (Rel. 16, Created)

DT 01-NOV-1990 (Rel. 16, Last sequence update)

DT 01-FEB-1996 (Rel. 33, Last annotation update)

DE Cubitus interruptus dominant protein.

GN C1-D.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI\_TaxID=7227;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=OREGON-R.

RX MEDLINE=90346286; PubMed=2166702;

RA Orenic T.V., Slusarski D.C., Kroil K.L., Holmgren R.A.;

RT "Cloning and characterization of the segment polarity gene cubitus

RT interruptus dominant of Drosophila.";

RL Genes Dev. 4:1053-1067(1990).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=OREGON-R.

RX MEDLINE=92146935; PubMed=1686006;

RA Berry A.J., Ajioka J.W., Kreilman M.;

RT "Lack of polymorphism on the Drosophila fourth chromosome resulting

RT from selection.";



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QY 189 TASASPPPLMD-----PVIN-----FDQEPSSVLSDD- 215
: : || ||:|
Db 211 SDTLSLOPLDCCANEIKVKLCKLGLGKFKFIEDITVLDNRNCRGTMKDEPNWVSTTS 270
: : || ||:|
QY 216 -----HHVILNEHVPFNSNLSONQTLNSNLTS 243
: : || ||:|
Db 271 PVVANDCGNILENNGTQAIYRNTLSLATDFIIRDFLVNFOCAPLDMNVSLQTLAQPI 330
: : || ||:|
QY 244 VSELKTPCKNPPLFTGSGASATLT 268
: : || ||:|
Db 331 VSSLND-----VGGAGETVT 347
: : || ||:|

RESULT 9
UVR_C.ECOLI
ID UVR_C.ECOLI STANDARD; PRT; 610 AA.
AC P07028; P76311;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Excinuclease ABC subunit C.
GN UVR_C OR B1913.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86176730; PubMed=3515318;
RA Sharma S., Stark T.F., Beattie W.G., Moses R.E.;
RT "Multiple control elements for the uvrC gene unit of Escherichia coli."
RL Nucleic Acids Res. 14:2301-2318(1986).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=84247323; PubMed=6330676;
RA Sancar G.B., Sancar A., Rupp W.D.;
RT "Sequences of the E. coli uvrC gene and protein."
RL Nucleic Acids Res. 12:4593-4608(1984).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=97251358; PubMed=9097040;
RA Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Kasai H., Kimura S., Kitagawa M., Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T., Saito N., Sampei G., Seki Y., Sivasubram S., Tagami H., Takeda J., Takemoto K., Wada C., Yamamoto Y., Horiuchi T.;
RT "A 460-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 40.1-50.0 min region on the linkage map."
RL DNA Res. 3:379-392(1996).
RN [5]
RP SEQUENCE OF 1-28 FROM N.A.
RX MEDLINE=87231005; PubMed=3295776;
RA Moolenaar G.F., van Sluis C.A., Backendorf C., van de Putte P.;
RT "Regulation of the Escherichia coli excision repair gene uvrC. Overlap between the uvrC structural gene and the region coding for a 24 kD protein."
RL Nucleic Acids Res. 15:4273-4289(1987).
RN [6]
RP SEQUENCE OF 604-610 FROM N.A.
RX MEDLINE=86111778; PubMed=3003065;

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RA Gopalakrishnan A.S., Chen Y.C., Temkin M., Dowhan W.;
RT "Structure and expression of the gene locus encoding the phosphatidylglycerophosphate synthase of Escherichia coli."
RL J. Biol. Chem. 261:1329-1338(1986).
CC -I- FUNCTION: THE ABC EXCISION NUCLEASE IS A DNA REPAIR ENZYME THAT CATALYZES THE EXCISION REACTION OF UV-DAMAGED NUCLEOTIDE SEGMENTS PRODUCING OLIGOMERS HAVING THE MODIFIED BASE(S). ATTACHES TO THE UVR_A-UVR_B COMPLEX, DISPLACING UVR_A, AND THE DAMAGED DNA STRAND IS NICKED ON BOTH SIDES OF THE DAMAGED SITE.
CC -I- SUBUNIT: CONSISTS OF THREE SUBUNITS; UVR_A, UVR_B AND UVR_C.
CC -I- SUBCELLULAR LOCATION: Cytoplasmic.
CC -I- SIMILARITY: BELONGS TO THE UVR_C FAMILY.
CC
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CC
CC EMBL; X03691; CAA27329.1; ALT_INIT.
CC EMBL; M24615; AAA24756.1; -.
CC EMBL; AE000284; AAC74980.1; ALT_INIT.
CC EMBL; D90832; BAA15733.1; -.
CC EMBL; X05398; CAA28983.1; -.
CC EMBL; M12299; AAA98753.1; -.
CC PIR; A22863; BVCEUC.
CC PIR; C24964; C24964.
CC ECO2DBASE; I065.0; 6TH EDITION.
CC EcoGene; EG11063; uvrC.
CC InterPro; IPR000445; HHH.
CC InterPro; IPR003583; HHH_1.
CC InterPro; IPR001943; UVR.
CC InterPro; IPR001162; UVR_C_2.
CC InterPro; IPR000305; UvrC_1.
CC Pfam; PF01541; Exci_endo_N; 1.
CC Pfam; PF00633; HHH; 2.
CC Pfam; PF02151; UVR; 1.
CC ProDom; PD005870; UVR_C_2; 1.
CC SMART; SM00465; GYc; 1.
CC SMART; SM00278; Hhh1; 2.
CC SOS response; Excision nuclease; DNA repair; Complete proteome.
FT CONFLICT 291 291 K -> E (IN REF. 3 AND 4).
SQ SEQUENCE 610 AA; 68187 MW; C347C4606FACB926 CRC64;

Query Match 4.8%; Score 85; DB 1; Length 610;
Best Local Similarity 25.7%; Pred. No. 6.3;
Matches 47; Conservative 17; Mismatches 63; Indels 56; Gaps 9;

QY 94 RATATGYWKATGKDRTI-----LRKGLVGMKRTLVFYOGRAPRGRKTD 137
: : || ||:| : || ||:|
Db 238 RVTEKQFVSNTGDDLDVIGVAFDAGMACVHVLFTRQGVLSRS-----YFPKVPGGTKLS 293
: : || ||:|
QY 138 WVMH-----EPRLOCHSHPPNHSLSPPKEDVLCRVFKNTEGVICRD-NMGSCFDETA 192
: : || ||:|
Db 294 EVETFFVQGYLQGSQ-----MRTLPGEILLDFNLS---DKTLA 330
: : || ||:|
QY 193 -SLPPLMDPYINFQEPSSVLSDDHHYI-----INEHVPFNSNLSONQTLNSNLTSVSEL 247
: : || ||:|
Db 331 DLSLSELAGRKINVTQKPR---GDRARYLKLARTNAATLTSKLSQQSTVHORLTALASVL 387
: : || ||:|

QY 248 KIP 250
: : ||
Db 388 KLP 390

RESULT 10
NPT1_YEAST
ID NPT1_YEAST STANDARD; PRT; 429 AA.
AC P39683; Q08626;
DT 01-FEB-1995 (Rel. 31, Created)

```

01-NOV-1997 (Rel. 35, Last sequence update)  
30-MAY-2000 (Rel. 39, Last annotation update)  
Probable nicotinate phosphoribosyltransferase (EC 2.4.2.11)  
(NAPRTase).  
GN NPRT1 OR YOR209C.  
OS Saccharomycetes cerevisiae (Baker's yeast).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.  
OX NCBI\_TaxID=4932;  
[1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=FL100;  
RA Lalo D., Doira C., Thuriaux P.;  
RL Submitted (JAN-1995) to the EMBL/GenBank/DBJ databases.  
[2]  
RN SEQUENCE FROM N.A.  
RP Hughes B., Pohl T.M.;  
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.  
[3]  
RN SEQUENCE OF 1-43 FROM N.A.  
RC STRAIN=FL100;  
RX MEDLINE=91296170; PubMed=8516295;  
RA Lalo D., Carles C., Sentenac A., Thuriaux P.;  
RT "Interactions between three common subunits of yeast RNA polymerases  
I and III.";  
RL Proc. Natl. Acad. Sci. U.S.A. 90:5524-5528(1993).  
CC -!- CATALYTIC ACTIVITY: Nicotinate D-ribonucleotide + diphosphate =  
nicotinate + 5-phospho-alpha-D-ribose 1-diphosphate.  
CC -!- PATHWAY: FIRST STEP IN PREISS-HANDLER PATHWAY LEADING TO THE  
SYNTHESIS OF NAD.  
CC -!- SIMILARITY: BELONGS TO THE NAPRTASE FAMILY.  
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-----  
DR EMBL; Z36878; CAA85352.1; -;  
DR EMBL; Z75117; CAA99424.1; -;  
DR EMBL; L11274; AAB59317.1; -;  
DR PIR; S48884; S48884.  
DR SGD; S0005735; NPRT1.  
DR TRANSFERASE; Glycosyltransferase.  
FT CONFLICT 131 137 YEIPLLS -> MRLSTV (IN REF. 1).  
FT CONFLICT 144 159 FKEVDIDWDYENQLEQ -> LIYTSGLRNHRO (IN  
REF. 1).  
FT CONFLICT 175 177 SEF -> RIH (IN REF. 1).  
FT CONFLICT 243 243 E -> EL (IN REF. 1).  
SQ SEQUENCE 429 AA; 49018 MW; F3F7941476C3398B CRC64;  
  
Query Match 4.8%; Score 84.5; DB 1; Length 429;  
Best Local Similarity 18.4%; Pred. No. 4.3;  
Matches 72; Conservative 56; Mismatches 140; Indels 123; Gaps 21;  
  
QY 3 TEEMKESISSMVEAKLP-----PGRFHPKDD-ELVCDVLMRSLNHRPP 49  
DB 66 TEEE-----EYLKQETPLPSAIVIKYISSNKLHPHEQISFTSEIEGKPHYKLG-- 118  
  
QY 50 LVLIQVDLNKCEPNDIPKMACVGGK-----DWFY---YSQDRKYAT----- 88  
DB 119 -ILVSGSWKOTILVEIPLLSLISEAYFKFVDIDWDYENQLEQAEKKAETLFDNGIRSEF 177  
QY 89 GLRTRNATAT-----GYWRAT--GKDRITLRGKLVGMKRTLVFYQ--GRAPGRKT-DW 138  
DB 178 GTRRRSLKAQDLIMQGITMKAVNGNPDR---NKSLLGTSNILLFAKKYGVKPIGTVAHEW 234  
QY 139 VMHEFRLOGSHHPNHSPPKEDWLCRVFHNKTEGVICRDNMGSCFDETSASLPPLM 198  
DB 235 VMGVASISDY---LHANKNAMDCWI--NTEGAKNAGLALTDTEGT--DDFLKSRFPYS 287

QY 199 DPVINFQDQ---EPSSYLSQ-DHHYIINEHVPCFSN-LSQNTLN----- 237  
DB 288 DAVGVGVQSDGDPVEYTKKISHHYHDVCLKPKFSKICYSDSLNVEKAITTYSHAAKENG 347  
QY 238 -----SNLNSVSELKIPCKNPPLFTGCGSASATLTGLDSCSDQMVLRALLSQT 290  
DB 348 LATFGTGTNTFNDFRKKSPQVKSEPL-----NIVIKLIE 382  
QY 291 IDGSLGPKESQSYGEGSSESLTLDIGIPSTV 321  
DB 383 VGNHAIKISDNLGK-----NMGDPAIV 405  
  
RESULT 11  
HAIR\_MOUSE  
ID HAIR\_MOUSE STANDARD; PRT; 1182 AA.  
AC Q61645;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Hairless protein.  
GN HR.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BA1B/C; TISSUE=SKIN;  
RX MEDLINE=94329587; PubMed=8052649;  
RA Cachon-Gonzalez M.B., Fenner S., Coffin J.M., Moran C., Best S.,  
RT Stoye J.P.;  
RL "Structure and expression of the hairless gene of mice.";  
RL Proc. Natl. Acad. Sci. U.S.A. 91:7717-7721(1994).  
CC -!- FUNCTION: MAY ACT AS A TRANSCRIPTION FACTOR THAT COULD ACT ON TO  
REGULATE ONE OF THE PHASES OF HAIR GROWTH.  
CC -!- SUBCELLULAR LOCATION: Nuclear.  
CC -!- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN BRAIN, HAIR  
FOLLICLES AND INTERFOLLICULAR EPIDERMIS. NO EXPRESSION IN  
DERMIS.  
CC -!- DISEASE: HR MUTATION PRODUCES A NUMBER OF PLEIOTROPIC EFFECTS  
INCLUDING STRUCTURAL ABNORMALITIES OF EPITHELIAL CELLS IN THE HAIR  
FOLLICLES, HAIR LOSS TOWARDS THE END OF THE FIRST HAIR GROWTH  
CYCLE, AND THE FAILURE OF SUBSEQUENT HAIR GROWTH CYCLES. OLDER  
MICE CARRYING AN HR MUTATION HAVE BEEN REPORTED TO POSSESS ALTERED  
RATIOS OF T-CELL-DEPENDENT B-CELL RESPONSES. MICE HOMOZYGOUS FOR  
HR MUTATION ARE UNIQUELY SENSITIVE TO UV AND CHEMICALLY INDUCED  
SKIN TUMORS.  
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-----  
DR EMBL; Z32675; CAA83587.1; -;  
DR MGD; MGI:96223; hr.  
DR InterPro; IPR003347; JmJC.  
DR Pfam; PF02373; JmJC; 1.  
KW Zinc-finger; DNA-binding; Nuclear protein; Transcription regulation;  
Metal-binding.  
FT ZN\_FING 595 620 C6-TYPE.  
FT DOMAIN 535 540 POLY-GLY.  
SQ SEQUENCE 1182 AA; 127182 MW; EFB0EE62AE81B40 CRC64;  
  
Query Match 4.8%; Score 84.5; DB 1; Length 1182;  
Best Local Similarity 23.0%; Pred. No. 17;  
Matches 59; Conservative 16; Mismatches 92; Indels 89; Gaps 11;



QY 111 LRKGLVGMKRTLVFYQGRAPRG--RKTDW-----VMHEFRLOGSHHP----- 151  
 Db 61 LPFCFLQGRKDTLSLVEGEGPRNGERKSGWLGKGLRWKEAMLAHPLAFCGACPPRYG 120  
 QY 152 ---PNHSLSPKEDWVLCRVFKHNTGVCIDRMNGSCFDEITASLPLMDPYINFDQEP 208  
 Db 121 PLIPEHSGGHKSPDPAFAPLH-----CPLETKILERAPFWVPTCLPPYL----- 167  
 QY 209 SSYLSDDHHYIINEHVPFCFNSLSQNTLSNLTNSVSLKIPCKNPNPLFTGSGS---AS 264  
 Db 168 -----MSSLPPRPYDWPLA-----PNPWVYSGSPKVP 197  
 QY 265 ATUTGLDSCSSQDMVLRALLSOLTKIDGSL-----GPKESQSYGE---G 306  
 Db 198 AFGLSGKGFVKHDPNILRPAKEPLAE-SGMLGLAPGGHLQACSESGPSLHQRDGETGAG 256  
 QY 307 SSESLL-TDIGIPSTV 321  
 Db 257 RQNLCPVFLGYPDTV 272

RESULT 12  
 PA2R\_RABIT  
 ID PA2R\_RABIT STANDARD; PRT: 1458 AA.  
 AC P49260;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE 180 kDa secretory phospholipase A2 receptor precursor (PLA2-R).  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OX NCBI\_TaxID:9986;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
 RC TISSUE=Skeletal muscle;  
 RX MEDLINE=94124484; PubMed=8294398;  
 RA Lambeau G., Ancian P., Barhanin J., Lazdunski M.;  
 RT "Cloning and expression of a membrane receptor for secretory  
 phospholipases A2";  
 RL J. Biol. Chem. 269:1575-1578(1994).  
 CC -1- FUNCTION: MAY HAVE A KEY ROLE IN NORMAL AND PATHOLOGICAL ACTIONS  
 CC OF SECRETORY PHOSPHOLIPASE A2. ALSO BINDS TO SNAKE PA2-LIKE  
 CC TOXINS.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- TISSUE SPECIFICITY: LUNG, SKELETAL MUSCLE, BRAIN, KIDNEY AND  
 CC HEART.  
 CC -1- SIMILARITY: CONTAINS 8 C-TYPE LECTIN FAMILY DOMAINS.  
 CC -1- SIMILARITY: CONTAINS 1 RICIN B-TYPE LECTIN DOMAIN.  
 CC -----  
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 CC -----  
 CC HSSL; U03455; AAC48402.1; -.  
 DR HSP; P02751; 2FN2.  
 DR InterPro: IPR000562; FN\_Type\_II.  
 DR InterPro: IPR000772; Ricin\_B\_lectin.  
 DR InterPro: IPR001304; lectin\_c.  
 DR Pfam: PF00040; fn2; 1.  
 DR Pfam: PF00059; lectin\_c; 8.  
 DR Pfam: PF00652; Ricin\_B\_lectin; 1.  
 DR PRINTS: PR00013; FNYPEII.  
 DR ProDom: PD000995; FN\_Type\_II; 1.  
 DR SMART; SM00034; CLECT; 8.  
 DR SMART; SM00059; FN2; 1.  
 DR SMART; SM00458; RICIN; 1.  
 DR PROSITE: PS00615; C-TYPE LECTIN\_1; 3.  
 DR PROSITE: PS50041; C-TYPE LECTIN\_2; 8.

DR PROSITE; PS00023; FIBRONECTIN\_2; 1.  
 DR PROSITE; PS00231; RICIN\_B\_LECTIN; 1.  
 KW Signal; Receptor; Transmembrane; Repeat; Glycoprotein; Lectin.  
 FT SIGNAL 1 23 POTENTIAL.  
 FT CHAIN 24 1458 180 KDA SECRETORY PHOSPHOLIPASE A2  
 RECEPTOR.  
 FT DOMAIN 24 1393 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 1394 1416 POTENTIAL.  
 FT DOMAIN 1417 1458 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 49 113 RICIN B-TYPE LECTIN.  
 FT DOMAIN 165 220 FIBRONECTIN TYPE-II.  
 FT DOMAIN 227 356 C-TYPE LECTIN 1 (LONG FORM).  
 FT DOMAIN 374 502 C-TYPE LECTIN 2 (LONG FORM).  
 FT DOMAIN 511 645 C-TYPE LECTIN 3 (LONG FORM).  
 FT DOMAIN 660 798 C-TYPE LECTIN 4 (LONG FORM).  
 FT DOMAIN 815 939 C-TYPE LECTIN 5 (LONG FORM).  
 FT DOMAIN 954 1098 C-TYPE LECTIN 6 (LONG FORM).  
 FT DOMAIN 1117 1231 C-TYPE LECTIN 7 (LONG FORM).  
 FT DOMAIN 1243 1376 C-TYPE LECTIN 8 (LONG FORM).  
 FT CARBOHYD 91 91 N-LINKED (GLCNAC... (POTENTIAL).  
 FT CARBOHYD 408 408 N-LINKED (GLCNAC... (POTENTIAL).  
 FT CARBOHYD 431 431 N-LINKED (GLCNAC... (POTENTIAL).  
 FT CARBOHYD 452 452 N-LINKED (GLCNAC... (POTENTIAL).  
 FT CARBOHYD 471 471 N-LINKED (GLCNAC... (POTENTIAL).  
 FT CARBOHYD 582 582 N-LINKED (GLCNAC... (POTENTIAL).  
 FT CARBOHYD 725 725 N-LINKED (GLCNAC... (POTENTIAL).  
 FT CARBOHYD 778 778 N-LINKED (GLCNAC... (POTENTIAL).  
 FT CARBOHYD 907 907 N-LINKED (GLCNAC... (POTENTIAL).  
 FT CARBOHYD 981 981 N-LINKED (GLCNAC... (POTENTIAL).  
 FT CARBOHYD 1054 1054 N-LINKED (GLCNAC... (POTENTIAL).  
 FT CARBOHYD 1106 1106 N-LINKED (GLCNAC... (POTENTIAL).  
 FT CARBOHYD 1121 1121 N-LINKED (GLCNAC... (POTENTIAL).  
 FT CARBOHYD 1130 1130 N-LINKED (GLCNAC... (POTENTIAL).  
 FT CARBOHYD 1319 1319 N-LINKED (GLCNAC... (POTENTIAL).  
 SQ SEQUENCE 1458 AA; 16719 MW; 686163066DAB9511 CRC64;

Query Match 4.8%; Score 84.5; DB 1; Length 1458;  
 Best Local Similarity 19.7%; Pred. No. 23;  
 Matches 59; Conservative 44; Mismatches 93; Indels 103; Gaps 16;

QY 23 FRFHPKDD-----ELVCDYLMR--RSLNHRPPLVLIQVDLNKCEPMDIPKACVGGKD 75  
 Db 822 YLFYHPSSESSSFEVCGWLRSDILTITSAHEQEFILSKI-----KALSKYGAN 870  
 QY 76 WYFYSQ-----RDKYATGRTNR---ATATGYWKATGKDR 109  
 Db 871 WWIGLQETANDELNRDGTPIVYQNDKDRSMNQSORCAFISITGLWD----- 923  
 QY 110 ILRKGKLVGM-----RKTLYFYQ-----GRAPGRKTDVVMHEFRLOGSHHPNHS 155  
 Db 924 --REECVSMPISCKRRTFWIEKEKDTPKQHGTCPKG---WLYFDYKCLLVNPKD-- 975  
 QY 156 LSSPKEDWLCRVPHKNTGVCIDRMNGSCFDE--TASASLPLMDPYIN---FDQSPSS 210  
 Db 976 -PSNWKNTQARDP-----CFDEGGTLVAIESEVEQAFIWNLFQQTNV 1019  
 QY 211 YL---SDHHYIINEHVPFCFNSLSQNTLSNLTNSVSELK-IP-----CKNPNPLFTG 260  
 Db 1020 WIGLQNDYKWLNGNPVAYSNWSPSDIINPTSYNTTADQKPIPLCALLSSNPNFHTG 1078

RESULT 13  
 YDTE\_SCHPO  
 ID YDTE\_SCHPO STANDARD; PRT: 337 AA.  
 AC O14216;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE Hypothetical 38.7 kDa protein C6B12.11 in chromosome I.  
 GN SPAC6B12.11.  
 OS Schizosaccharomyces pombe (Fission yeast).  
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;





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QY 130 -----APR-----GRKTDVNH-----EFLRQSHHPNHSLSPKED----- 162
DB 275 ILAALMCAPRSVYSWDIVIQVGNKLFKDRKQSLDLSVHETSQEPFLPSKDDINSAH 334
QY 163 --WVLCRVFHKNTGVITCRDNMGSCFDETSASLPLMDPYINFDQEPSY----- 211
DB 335 SLGVEAYINQFQQVLVRDGGKKTDEA-----NPFANEGEIASVAYRYRWK 385
QY 212 LSDHHYI-----INEHVPFCSNLSQNTLSNLTNSVSELKI 249
DB 386 LDDNMHLVARCELOSVADLNNQRSLFTLNALNEFDPKYGVDMRQKLE---TORGAVLAT 442
QY 250 PCKNPNPLFTGGSSASAVLTGLD 271
DB 443 ELKNGNKLAKWTAQALLANAD 464

RESULT 15
ENV_IPMAE
ID ENV_IPMAE STANDARD; PRT; 584 AA.
AC P31789;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE ENV polyprotein precursor (Coat polyprotein) [Contains: Surface
DE protein; Transmembrane protein].
GN ENV.
OS Mouse intracisternal a-particle (IAP-MIAE).
OC Viruses; Retroviral viruses; Retroviridae; Intracisternal A-particles.
OX NCBI_TaxID=11932;
RN [1]
RP
RX MEDLINE=92015460; PubMed=1920613;
RA Reuss F.U., Schaller H.C.;
RT "cDNA sequence and genomic characterization of intracisternal
RT A-particle-related retroviral elements containing an envelope
RT gene.";
RL J. Virol. 65:5702-5709(1991).
CC -1- MISCELLANEOUS: READTHROUGH OF THREE TERMINATORS OCCURS: UGA
CC BETWEEN CODONS FOR 71-THR AND 72-ALA, UGA BETWEEN CODONS FOR
CC 111-HIS AND 112-ARG, AND UAA BETWEEN CODONS FOR 394-VAL AND
CC 395-SER.
CC -1- MISCELLANEOUS: THIS PARTICLE IS A DECEPTIVE RETROVIRUS.
CC -----
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CC -----
CC EMBL; M73818; -; NOT_ANNOTATED_CDS.
CC PIR; A41305; VCMSTA.
KW Coat protein; Glycoprotein; Polyprotein; Transmembrane; Signal.
FT SIGNAL 1 25
FT CHAIN 26 584 ENV POLYPROTEIN.
FT CHAIN 26 362 SURFACE PROTEIN.
FT CHAIN 363 584 TRANSMEMBRANE PROTEIN.
FT TRANSMEM 527 547 POTENTIAL.
FT CARBOHYD 58 58 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 77 77 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 98 98 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 129 129 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 140 140 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 147 147 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 230 230 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 285 285 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 311 311 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 319 319 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 463 463 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 469 469 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 481 481 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 501 501 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 584 AA; 65024 MW; 180CCAF8F14ACD6 CRC64;

Query Match 4.7%; Score 82.5; DB 1; Length 584;
Best Local Similarity 22.2%; Pred. No. 9.9;
Matches 48; Conservative 24; Mismatches 63; Indels 81; Gaps 11;

QY 134 RKTDMWHFRLQSGSHHPNHS-----LSPK-----EDWVLCRVFHKNTGVIT----- 177
DB 134 QEVNWV-----NGTFLPPNFSKDEHLHQPKIAPHCSLED-----EGLLPWSD 176
QY 178 CRDNMGSCFDETSASLPLM--DPVINFDQPSVYSLDDHHYIINEHVPFCSNLSQNT 235
DB 177 COSSIIRWVDQSKTFSFSFNIMDDPEKEVMMKGLFIQDFRMHPFKWVLCVNGS----- 232
QY 236 LNSNLTVSVSELKIPCKNPNPPL-FTGSA--SATLTGLDSFCSSDQMYLRALLSOLTQID 292
DB 233 -----CTELNPLIFIQGGAVGKASFTGISRAQY----- 261
QY 293 GSLGPKESOSYG-----EGSSESLLTDIGIPST 320
DB 262 WGIHDASQDSYGYTNTSVEITGFNKTLYNQINYPST 297
```

Search completed: July 15, 2002, 07:00:14  
Job time: 206 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: July 15, 2002, 06:57:08 ; Search time 29.23 seconds  
(without alignments)

1917.563 Million cell updates/sec

Title: US-09-889-926-2

Perfect score: 1757

Sequence: 1 METEEMKESSISWEAKLP.....EGSSESLTDTGIPSTVWNC 324

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_19.\*

- 1: sp\_archaea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_mhc.\*
- 8: sp\_organelle.\*
- 9: sp\_phage.\*
- 10: sp\_plant.\*
- 11: sp\_rodent.\*
- 12: sp\_virus.\*
- 13: sp\_vertebrate.\*
- 14: sp\_unclassified.\*
- 15: sp\_rvirus.\*
- 16: sp\_bacteriap.\*
- 17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Query	Score	Match	Length	ID	Description
1	1757	100.0	324	10	Q9SE10	Q9se10 arabidopsis
2	1579.5	89.9	309	10	Q9SGS9	Q9sgs9 arabidopsis
3	967	56.2	279	10	Q9LS11	Q9ls11 arabidopsis
4	946	53.8	299	10	Q93XA7	Q93xa7 phaseolus v
5	557	31.7	329	10	Q9FLR3	Q9flr3 arabidopsis
6	552.5	31.4	327	10	Q40880	Q40880 petunia hyb
7	548	31.2	336	10	Q9FLJ2	Q9flj2 arabidopsis
8	545.5	31.0	335	10	Q9FK44	Q9fk44 arabidopsis
9	544	31.0	375	10	Q04017	Q04017 arabidopsis
10	542	30.8	331	10	Q9SC68	Q9sc68 oryza sativ
11	542	30.8	331	10	Q9SM90	Q9sm90 oryza sativ
12	536.5	30.5	334	10	Q9S851	Q9s851 arabidopsis
13	535.5	30.5	334	10	Q9LS50	Q9ls50 arabidopsis
14	533	30.3	318	10	Q9LJW3	Q9ljw3 arabidopsis
15	532.5	30.3	338	10	Q9SQQ6	Q9sqq6 arabidopsis
16	519	29.5	285	10	Q9FKA0	Q9fka0 arabidopsis

17	517	29.4	324	10	Q9AV06	Q9av06 oryza sativ
18	512	29.1	310	10	Q9PRV4	Q9prv4 arabidopsis
19	512	29.1	337	10	Q9LIL8	Q9lil8 arabidopsis
20	505.5	28.8	316	10	Q9ZQ25	Q9zq25 arabidopsis
21	500	28.5	320	10	Q9FTY0	Q9fty0 oryza sativ
22	491.5	28.0	365	10	Q9SL41	Q9sl41 arabidopsis
23	477	27.1	351	10	Q9ZR22	Q9zr22 triticum sp
24	473	26.9	298	10	Q9SLK1	Q9slk1 arabidopsis
25	472.5	26.9	334	10	Q9M274	Q9m274 arabidopsis
26	470.5	26.8	324	10	Q9C8W9	Q9c8w9 arabidopsis
27	466	26.5	256	10	Q93XA6	Q93xa6 phaseolus v
28	461	26.2	317	10	Q9LDY8	Q9ldy8 arabidopsis
29	459.5	26.2	399	10	Q81033	Q81033 arabidopsis
30	458.5	26.1	418	10	Q9SI80	Q9si80 arabidopsis
31	458	26.1	316	10	Q9MBC6	Q9mbc6 oryza sativ
32	456.5	26.0	348	10	Q9LVA1	Q9lva1 arabidopsis
33	456	26.0	377	10	Q65508	Q65508 arabidopsis
34	456	26.0	418	10	Q9ZVH0	Q9zvho arabidopsis
35	453.5	25.8	631	10	Q9SRZ8	Q9srz8 arabidopsis
36	452.5	25.8	297	10	Q93VY3	Q93vy3 arabidopsis
37	449.5	25.6	395	10	Q9SNM6	Q9snm6 oryza sativ
38	446.5	25.4	341	10	Q9SV87	Q9sv87 arabidopsis
39	446.5	25.4	349	10	Q9SOL0	Q9sol0 lycopersico
40	444	25.3	337	10	Q9FIW5	Q9fiw5 arabidopsis
41	442	25.2	246	10	Q9LSH5	Q9lsh5 arabidopsis
42	439.5	25.0	301	10	Q948Z2	Q948z2 solanum tub
43	439	25.0	320	10	Q9ZNU2	Q9znu2 arabidopsis
44	438.5	25.0	358	10	Q9LP17	Q9lp17 arabidopsis
45	437.5	24.9	476	10	Q9FFI5	Q9ffi5 arabidopsis

#### ALIGNMENTS

RESULT 1

Q9SE10	ID	Q9SE10	PRELIMINARY;	PRT;	324 AA.
AC	Q9SE10;				
DT	01-MAY-2000 (TREMBLrel. 13, Created)				
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)				
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)				
DE	NAC1 (F14JL6.32).				
GN	NAC1.				
OS	Arabidopsis thaliana (Mouse-ear cross).				
OC	Eukaryota; Viridiplantae; Streptophyta;				
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;				
OC	eurosid II; Brassicales; Brassicaceae; Arabidopsis.				
OX	NCBI_TaxID=3702;				
RN	[1]				
RC	SEQUENCE FROM N.A.				
RC	STRAIN=CV. LANDSBERG;				
RA	Xie Q., Chua N.H.;				
RT	"Arabidopsis NAC1 transduces auxin signal to promote later root development";				
RL	Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RA	Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S., Kim C., Altafi H., Bei Q., Chin C., Chou J., Choi E., Conn L., Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B., Lee J., Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A., Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A., Ecker J.R.;				
RT	"Genomic sequence for Arabidopsis thaliana BAC F14JL6 from chromosome I.,"				
RL	Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RA	Ecker J.R.;				
RL	Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.				
RN	[4]				
RP	SEQUENCE FROM N.A.				

RA Ecker J.R.;  
 RL Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RA Ecker J.R.;  
 RL Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RA Ecker J.R.;  
 RL Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.  
 RN [7]  
 RP SEQUENCE FROM N.A.  
 RA Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,  
 Kian S., Kim C., Altai H., Bel B., Chin C., Chiou J., Choi E.,  
 Conn L., Conway A., Gonzalez A., Hansen N., Howling B., Koo T., Lam B.,  
 Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N.,  
 Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,  
 Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N.,  
 Theologis A., Ecker J.;  
 RL Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AF198054; AAF21437.1; -;  
 DR EMBL; AC002304; AAF79328.1; -;  
 DR InterPro; IPR003441; NAM.  
 DR Pfam; PF02365; NAM; 1.  
 SQ SEQUENCE 324 AA; 36569 MW; C70ED705D1A6957 CRC64;

Query Match 100.0%; Score 1757; DB 10; Length 324;  
 Best Local Similarity 100.0%; Pred. No. 6.7e-161;  
 Matches 324; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 METEEMKESISSWVEAKLPFGFRHPKDDDELCDYLMRRSLHNNHRRPPLVLIQVDLNC 60  
 Db 1 METEEMKESISSWVEAKLPFGFRHPKDDDELCDYLMRRSLHNNHRRPPLVLIQVDLNC 60  
 QY 61 EPWDIPKMACVGKDWYFYSDRDKYATGLRTNRATATGYWKATGKDRITLKGK 120  
 Db 61 EPWDIPKMACVGKDWYFYSDRDKYATGLRTNRATATGYWKATGKDRITLKGK 120  
 QY 121 KTLVYQGRAPGRKTDWYMHFRLOGSHHPNHLSSPKEDWVLCRVFHKNTGVC 180  
 Db 121 KTLVYQGRAPGRKTDWYMHFRLOGSHHPNHLSSPKEDWVLCRVFHKNTGVC 180  
 QY 181 NMGSCFDEATASALPMDPYINFDQEPSSYLSDDHHYIINEHVPCFNSLSONQ 240  
 Db 181 NMGSCFDEATASALPMDPYINFDQEPSSYLSDDHHYIINEHVPCFNSLSONQ 240  
 QY 241 TNSVSELKIPCKNPPLFTGGSSATLTGLDSCSDQVLRALLSOLTKIDGSLGPKES 300  
 Db 241 TNSVSELKIPCKNPPLFTGGSSATLTGLDSCSDQVLRALLSOLTKIDGSLGPKES 300  
 QY 301 QSYGEGSSSESLTLDIGIPSTVWNC 324  
 Db 301 QSYGEGSSSESLTLDIGIPSTVWNC 324

RESULT 2  
 Q9SGS9 PRELIMINARY; PRT; 309 AA.  
 ID Q9SGS9  
 AC Q9SGS9  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DE T6H22.19 PROTEIN.  
 GN T6H22.19.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Federspiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F.,

RA Altai H., Nguyen M., Lam B., Buehler E., Dunn P., Gonzalez A.,  
 Kremenetskaia I., Kim C., Lenz C., Li J., Liu S., Luros S.,  
 RA Schwartz J., Shinn P., Toriumi M., Vysotskaia V.S., Walker M., Yu G.,  
 RA Ecker J., Theologis A., Davis R.W.;  
 RL Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AC009894; AAF02847.1; -;  
 DR InterPro; IPR003441; NAM.  
 DR Pfam; PF02365; NAM; 1.  
 SQ SEQUENCE 309 AA; 34715 MW; 2A263CD213E44688 CRC64;

Query Match 89.9%; Score 1579.5; DB 10; Length 309;  
 Best Local Similarity 91.8%; Pred. No. 7.8e-144;  
 Matches 302; Conservative 0; Mismatches 2; Indels 25; Gaps 3;

QY 1 METEEMKESISSWVEAKLPFGFRHPKDDDELCDYLMRRSLHNNHRRPPLVLIQVDLNC 60  
 Db 1 METEEMKESISSWVEAKLPFGFRHPKDDDELCDYLMRRSLHNNHRRPPLVLIQVDLNC 60  
 QY 61 EPWDIP-----KMACVGKDWYFYSDRDKYATGLRTNRATATGYWKATGKDRITLKGK 115  
 Db 61 EPWDIPMYNTTKRVCV-----QDRKYATGLRTNRATATGYWKATGKDRITLKGK 111  
 QY 116 LVGMKRTLVFYQGRAPGRKTDWYMHFRLOGSHHPNHLSSPKEDWVLCRVFHKNTG 175  
 Db 112 LVGMKRTLVFYQGRAPGRKTDWYMHFRLOGSHHPNHLSSP-----KNTEG 160  
 QY 176 VICRDNMGSCFDEATASALPMDPYINFDQEPSSYLSDDHHYIINEHVPCFNSLSONQ 235  
 Db 161 VICRDNMGSCFDEATASALPMDPYINFDQEPSSYLSDDHHYIINEHVPCFNSLSONQ 220  
 QY 236 LNSLNTSVSELKIPCKNPPLFTGGSSATLTGLDSCSDQVLRALLSOLTKIDGSL 295  
 Db 221 LNSLNTSVSELKIPCKNPPLFTGGSSATLTGLDSCSDQVLRALLSOLTKIDGSL 280  
 QY 296 GPKESQSYGEGSSSESLTLDIGIPSTVWNC 324  
 Db 281 GPKESQSYGEGSSSESLTLDIGIPSTVWNC 309

RESULT 3  
 Q9LSI1 PRELIMINARY; PRT; 279 AA.  
 ID Q9LSI1  
 AC Q9LSI1  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE NAM (NO APICAL MERISTEM) PROTEIN-LIKE.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OX eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=COLUMBIA;  
 RA Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.;  
 RL Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=COLUMBIA;  
 RX MEDLINE=20277480; PubMed=10819329;  
 RA Nakamura Y.;  
 RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence  
 RT features of the regions of 4,504,864 bp covered by sixty pl and TAC  
 RT clones";  
 RL DNA Res. 7:131-135(2000).  
 DR EMBL; AB026645; BAB02506.1; -;  
 DR InterPro; IPR003441; NAM.  
 DR Pfam; PF02365; NAM; 1.  
 SQ SEQUENCE 279 AA; 31946 MW; 376EE552927C416 CRC64;

Query Match	56.2%;	Score 987;	DB 10;	Length 279;
Best Local Similarity	62.8%;	Pred. No. 7.5e-87;		
Matches 203;	Conservative 24;	Mismatches 46;	Indels 50;	Gaps
QY	4	EEMKESSISWVAKLPPGFRFHPKDELVCYDLMRRSLNNHRPPLVLIQVDLNKCEPW 63		
Db	3	ETENKGSISWVEANLPPGFRFHPKDELVCYDLMRRSTVRSIQ-PVVLIDVDLNKCEPW 61		
QY	64	DIPKMACVGGKDWFFYSORDRKVATGLRTNRATATGYWKATGKDRITILRKGKLVGMKRTL 123		
Db	62	DIQTARVGGKEWFFYSQDRKVTATGYRTNRATATGYWKATGKDRAIQRNGGLVGMKRTL 121		
QY	124	VFYQGRAPRGKTDWMVHFEPLQGS--HHPNHSLSPPKEDWVLCRVFHKNTGCVICRDN 181		
Db	122	VFYGRSPKGRKTDWMVHFEPLQGLLHSPN---SLEEWVLCRVFHKNSNGDIDDI 177		
QY	182	MGSCFDETAASLPLMDPYINFDQBPSSYLSDDHHYIINEHVPCFS-NLSQNOTLNSNL 240		
Db	178	TRSCSDATASA---FMDSYINP-----DHHIILNQHVPCFSNNLSHNOTQSG 223		
QY	241	TNSVSELKIPKPNPLTGGSASATILGLDSCSDQMWLRALLSOLTKIDGSLGPKES 300		
Db	224	IS-----KNSSPLFN-----ASPDMLRLTLLSOLTK-----KVEES 255		
QY	301	QSYGEGSSSELTDIGIPSTVWN 323		
Db	256	QSRGDGSSSELTDIGIPSHAWN 278		
RESULT	4			
QY	93XA7	PRELIMINARY; PRT; 299 AA.		
ID	Q93XA7			
AC	Q93XA7			
DT	01-DEC-2001 (TrEMBLrel. 19, Created)			
DT	01-DEC-2001 (TrEMBLrel. 19, Last sequence update)			
DT	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)			
DE	NAC DOMAIN PROTEIN NAC1.			
OS	Phaseolus vulgaris (kidney bean) (French bean).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;			
OC	eurosid1; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Phaseolus.			
OX	NCBI_Taxid=3885;			
RP	SEQUENCE FROM N.A.			
RA	STRAIN=CV. RED KIDNEY; TISSUE=LEAF ABSCISSION ZONE;			
RC	Whitelaw C.A., Lyssenko N.N., Thai V.K., Nath P., Tucker M.L.;			
RT	"Functional analysis of regulatory elements in the gene promoter for			
RT	an abscission-specific cellulase from bean (Phaseolus vulgaris) and			
RT	characterization of candidate transcription factors.";			
RL	Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AF402602; AAK84883.1; -.			
SQ	SEQUENCE 299 AA; 33877 MW; 028D011BE405327D CRC64;			
Query Match	53.8%;	Score 946;	DB 10;	Length 299;
Best Local Similarity	60.2%;	Pred. No. 7.3e-83;		
Matches 192;	Conservative 44;	Mismatches 55;	Indels 28;	Gaps
QY	10	SSISWVEAKLPPGFRFHPKDELVCYDLMRRSLNNHRPPLVLIQVDLNKCEPWDPKMA 69		
Db	2	SNISWVEAKLPPGFRFHPKDELVCYDLMKKLTTHND---SLIMIDVDLNKCEPWDPETA 58		
QY	70	CVGCKDWFFYSQDRKVTATGLRTNRATATGYWKATGKDRITILRKGKLVGMKRTLVFYQGR 129		
Db	59	CVGCKDWFFYQDRKVTATGLRTNRATATGYWKATGKDRILRKGKLVGMKRTLVFYQGR 118		
QY	130	APGRKTDWMVHFEPLQGSHPHPNHSLSPPKEDWVLCRVFHKNTGCVICRDNMGSCFDE 189		
Db	119	APGRKTEWVHFEPLQGSHPHPNHSLSPPKEDWVLCRVFHKNTGCVICRDNMGSCFDE 175		
QY	190	ASASLPLMDPYINFDQBPSSYLSDDHHYIINEHVPCFSNLSONQT--LNSNLTVNSVSEL 247		
Db	176	GSSSLPALMDYSITFQTOA-----HADEFQVPCFSIFSONQANPTFNHMTTMEPKL 228		

DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)  
DT 01-DEC-2001 (TREMELrel. 19, Last annotation update)  
DE NAM GENE.  
GN NAM.  
OS Petunia hybrida (Petunia).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
OC Asteridae; euasterids I; Solanales; Solanaceae; Petunia.  
OX NCBI\_TaxID=4102;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=W137, AND W138; TISSUE=LEAF, AND CARPEL;  
RX MEDLINE=96200768; PubMed=8612269;  
RA Souer E., van Houwelingen A., Kloos D., Mol J., Koes R.;  
RT "The no apical meristem gene of Petunia is required for pattern  
RT formation in embryos and flowers and is expressed at meristem and  
RT primordia boundaries."  
RL Cell 85:159-170(1996).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=W138; TISSUE=CARPEL;  
RA Souer E.J.;  
RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=W138; TISSUE=CARPEL;  
RA Souer E.J.;  
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; X92204; CAA63101.1; -.  
DR EMBL; X92205; CAA63102.2; -.  
DR InterPro; IPR003441; NAM.  
DR Pfam; PF02365; NAM; 1.  
SQ SEQUENCE 327 AA; 36788 MW; 94C428A0176A8B3E CRC64;

Query Match 31.4%; Score 552.5; DB 10; Length 327;  
Best Local Similarity 42.8%; Pred. No. 6.3e-45;  
Matches 127; Conservative 42; Mismatches 69; Indels 59; Gaps 12;

QY 16 EAKLPGRFHPKDDDELCDYLMRSLHNNHRRPPLVLQVLDLKNCEPDIPKMACVGGKD 75  
Db 11 DSNLPPGFRHPTDELIYYLLKVLDSNF--TGRAIAEVDLKNCEPDLPEKAMGKE 69

QY 76 WFYISQDRKYATGLTRNATATGYWKATGKDRITL--RKGLVGMKRTLVFYQGRAPRG 133  
Db 70 WYFSLRDRKYPTGLTRNATAGYWKATGKDRYISKTSALVCMKKTLYFYGRAPRG 129

QY 134 RKTDDWVHFERLOGSHHPNHSLS-SPKEDWVLCRVFKHNTGEGVTCRDNMG-----SCFD 187  
Db 130 EKSNNWVHFERLDGKF--AYHVISRSKDEWVISRVFKSCSTVGTTSNGGKKRLNSSFN 187

QY 188 -----ETASASLPLMD--PYINFQEPSSYLSDDHHYIINEHVPCFSNL----- 230  
Db 188 NMVQEVSSPSVSLPPLLESSPYN--TATSAASK-----KEHVSCFSTISPTSPDPS 239

QY 231 -----SQNTLNSLTNSVSELKIPCKN-----PN-----PFTGGSAS 264  
Db 240 SVFDISSNSNTLHSLPAPSFSAILDPSFTRNSVFPSPSLRSLQENLHLPFGGTS 296

RESULT 7  
Q9FLJ2 ID Q9FLJ2 PRELIMINARY; PRT; 336 AA.  
AC Q9FLJ2;  
DT 01-MAR-2001 (TREMELrel. 16, Created)  
DT 01-MAR-2001 (TREMELrel. 16, Last sequence update)  
DT 01-DEC-2001 (TREMELrel. 19, Last annotation update)  
DE NAM (NO APICAL MERISTEM)-LIKE PROTEIN.  
GN MFB13.2.  
OS Arabidopsis thaliana (Mouse-ear cross).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC euroids II; Brassicales; Brassicaceae; Arabidopsids.

OX NCBI\_TaxID=3702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=COLUMBIA;  
RX MEDLINE=98290546; PubMed=9628582;  
RA Sato S., Kaneko T., Kotani H., Nakamura Y., Asamizu E., Miyajima N.,  
RA Tabata S.;  
RT "Structural analysis of Arabidopsis thaliana chromosome 5. IV.  
RT Sequence features of the regions of 1,456,315 bp covered by nineteen  
RT physically assigned pl and TAC clones."  
RL DNA Res. 5:41-54(1998).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC Southwick A., Karlin-Neumann G., Nguyen M., Lam B., Miranda M.,  
RA Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,  
RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,  
RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,  
RA Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,  
RA Ecker J., Theologis A., Davis R.W.;  
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB010073; BAB08499.1; -.  
DR EMBL; AY054644; AAK96835.1; -.  
DR InterPro; IPR003441; NAM.  
DR Pfam; PF02365; NAM; 1.  
SQ SEQUENCE 336 AA; 38472 MW; 2595C4FBD8B0680 CRC64;

Query Match 31.2%; Score 548; DB 10; Length 336;  
Best Local Similarity 37.3%; Pred. No. 1.8e-44;  
Matches 137; Conservative 53; Mismatches 101; Indels 76; Gaps 14;

QY 1 MET-----EEMKESISMVEAKLPGRFHPKDDDELCDYLMRSLHNNHRRPPLVLQ 54  
Db 1 METFCGFGKEEQMD-----LPGFRHPTDELIYYLLKVLDSNFSAK-AIGE 50

QY 55 VDLNKCPEWDIPKMACVGGKDWYFYSDRKYATGLTRNATATGYWKATGKDRITLKG 114  
Db 51 VDLNKCPEWLPWMAKGEKWEYFCVDRKYPTGLTRNATAGYWKATGKDRITLKG 110

QY 115 KLVMKRTLVFYQGRAPRGKRTDWMHFEFLQG---SHPPNHSLSPPKEDWVLCRVFKH 171  
Db 111 SLVGMKKTLYFYGRAPRGKRTDWMHFEFLQG---SHPPNHSLSPPKEDWVLCRVFKH 166

QY 172 NTEG-----VICRDNMGSCFDETSASLPLMD--PYINFQEPSSYLSDDHHYIINE 222  
Db 167 SAGGKKTPISSLRIGSLGTDENPSL--LPSLTSSPYNDKTKTEPVY----- 212

QY 223 HVPFCSN-LSQNG--TUNSNLTNSVSELKIPCKNPNPLFTGGSASATLTGLDSCSSDQM 279  
Db 213 -VPCFSNQTQNOGTTLNCFFSSPVLNSIQADIFHRIPLYQTSLOYSWNLQSPVLTOEHS 271

QY 280 VLRALL-----SOLTKI-----DGLGPKESQSVGEGSSSLLTDIG 316  
Db 272 VLHAMENNRQSLKTMVSVQETGVSTDMTDTISSDFEFGKRRDFDQEDPSSSTGPVDL- 330

QY 317 IPSTVMN 323  
Db 331 --EPFVN 335

RESULT 8  
Q9FK44 ID Q9FK44 PRELIMINARY; PRT; 335 AA.  
AC Q9FK44;  
DT 01-MAR-2001 (TREMELrel. 16, Created)  
DT 01-MAR-2001 (TREMELrel. 16, Last sequence update)  
DT 01-JUN-2001 (TREMELrel. 17, Last annotation update)  
DE NAM (NO APICAL MERISTEM)-LIKE PROTEIN.  
OS Arabidopsis thaliana (Mouse-ear cross).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC euroids II; Brassicales; Brassicaceae; Arabidopsids.  
OX NCBI\_TaxID=3702;











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OM protein - protein search, using sw model

Run on: July 15, 2002, 06:52:53 ; Search time 33.36 Seconds  
(without alignments)  
1078.774 Million cell updates/sec

Title: US-09-889-926-2  
Perfect score: 1757  
Sequence: 1 METFEEMKESSISWPAKLP.....EGSSELLTDIGIPSTVWNC 324

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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10: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AAL1989.DAT.*
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22: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA2001.DAT.*
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Query	Score			Length			DB	ID	Description
		Match	Match	Match	Match	Match	Match			
1	1757	100.0	324	21	AAB15081	Arabidopsis thalia				
2	1561	88.8	287	21	AAG22847	Arabidopsis thalia				
3	1391	79.2	257	21	AAG17253	Arabidopsis thalia				
4	1391	79.2	257	21	AAG22848	Arabidopsis thalia				
5	1112	63.3	206	21	AAG17254	Arabidopsis thalia				
6	1112	63.3	206	21	AAG22849	Arabidopsis thalia				
7	1112	63.3	206	21	AAG45796	Arabidopsis thalia				
8	1112	63.3	206	21	AAG45925	Arabidopsis thalia				
9	997	56.7	185	21	AAG17255	Arabidopsis thalia				
10	997	56.7	185	21	AAG45797	Arabidopsis thalia				
11	997	56.7	185	21	AAG45926	Arabidopsis thalia				

## ALIGNMENTS

RESULT	1	
AAAB15081	AAAB15081	
ID	AAAB15081	standard; Protein; 324 AA.
XX	XX	
XX	AAAB15081;	
XX	XX	
XX	19-DEC-2000	(first entry)
DDT	DDT	
DE	DE	
DE	Arabidopsis	NAC1 protein.
DE	XX	
KW	NAC 1;	genetically modified; larger.
XX	XX	
XX	Arabidopsis	thaliana.
XX	XX	
PN	WO200047742-A1.	
XX	XX	
XX	17-AUG-2000.	
XX	XX	
PF	11-FEB-1999;	99WO-SG00011.
XX	XX	
XX	11-FEB-1999;	99WO-SG00011.
XX	XX	
PP	(MOLE-)	INST MOLECULAR AGROBIOLOGY.
PI	PI	
PI	Xie Q,	Chua N;
XX	XX	
DR	WPI;	2000-506095/45.
DR	N-PSDB:	AAA89936.

Isolated NAC1 gene sequence from *Arabidopsis thaliana* is used to produce transgenic plants which are larger than the wild type versions.

Claim 2; page 20-21; 35pp; English.

XX The present sequence is Arabidopsis thaliana NAC1 protein. The NAC1 gene  
CC belongs to the NAC family of genes which may play a role in patterning  
CC of the shoot and floral meristem. This gene was isolated from an A.  
CC thaliana cDNA library expressed in Schizosaccharomyces pombe cells. The  
CC NAC1 gene may be used for making a genetically altered plant which is  
CC larger than a wild type version of the plant by overexpressing NAC1. The  
CC modified plant produces larger leaves, larger roots and more lateral  
CC roots than the wild type version.  
XX  
SQ Sequence 324 AA;

Query Match 100.0%; Score 1757; DB 21; Length 324;  
Best Local Similarity 100.0%; Pred. No. 5.6e-172;  
Matches 324; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEETEENKESISWEAKLPGRFRHPKDELVCYDLMRSLHNNRPLVLQVDLNC 60  
DB 1 meteeemkessismveaklppgrfrfhpkdldvcdylmrslhnnhrplvlqvdlnc 60  
QY 61 EPWDIPKMACVGKDWYFSORDKYATGLRTNRATATGYWKATGKDRILRKGKLVGMR 120  
DB 61 epwdipkmacvgkdwfyfsqrkdyatglrtnratatgywkatkdrtilrkgklvgmr 120  
QY 121 KTLVFOGRAPGRKTDVWMEFRLOGSHHPNHSLSPEKDWVLCRVFHKTEGVICRD 180  
DB 121 ktlvfyggrapgrktdvwmhefrlogshhpnhsllspkdwvlcervfhkategvicrd 180  
QY 181 NMGSCDETASLPLMDPYINFDOEPSSYLSDDHHYIINEHVPCFNSLQNQTLNSNL 240  
DB 181 nmgsctdetasallplmdpyinfdepsyslstdhhyiinehvpfnslnqntlnsni 240  
QY 241 TNSVSELKIPCKNPPLFTGGASATLTLGLDSCSDQMVLRALLSOLFKIDGSLGPKES 300  
DB 241 tnsvelkipcknpplftggasaatlgltdscsdqmvlrallsolfkidgslgpkgs 300  
QY 301 QSYGEGSSELLTDIGIPSTVWNC 324  
DB 301 qsygegsseslltdigipstvnc 324

RESULT 2  
AAG22847  
ID AAG22847 standard; Protein: 287 AA.  
XX  
AC AAG22847;  
XX  
DT 17-OCT-2000 (first entry)  
XX  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 25931.  
XX  
KW Protein identification; signal transduction pathway; metabolic pathway;  
KW hybridisation assay; genetic mapping; gene expression control; promoter;  
KW termination sequence.  
XX  
OS Arabidopsis thaliana.  
XX  
PN EP1033405-A2.  
XX  
PD 06-SEP-2000.  
XX  
PF 25-FEB-2000; 2000EP-0301439.  
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Query Match

88.8%; Score 1561; DB 21; Length 287;

Best Local Similarity 100.0%; Pred. No. 6.7e-152;

Matches 287; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	1	mrrslhnnhrpplvliqvdlnkcepdipkmacvggkdwfyfsqrdkrkyatglrtnrata	60

Qy	98	TGYWKATGKDETIILRKGLYGMKRTLVFYOGRAPRGKTDVWVHEFRLOGSHPPNHSLS	157
Db	61	tgylwkatgkdrtilrkglvgrmrktlvfygrrgrkrtdvwmhefrlqshppnhsls	120

Qy	158	SPKEDWVLCRVFHKNTGVICRDNMGSFCDETASASLPPLMDPYINFDPSPSYLSDHH	217
Db	121	spkedwvlcrvfhkntegvicrdnmgsfcdetasaslpplmdpyinfdpespylsdhh	180

Qy	218	YIINEHVPFCFNLSONQTLNSLTNSYSELKIPCKNPPLFTGSGASATLTGLDSFCSSD	277
Db	181	ylinehvpfcfnlsnqgtlnsltnsvselkipcknpplftgsgasatltgldsfcssd	240

Qy	278	QWLRALLSOLTKIDGSLGPKESQSGEGSSESLITDIGIPSTVWNC	324
Db	241	qmwlrallsqitkidgslgpkessqsgesessltdigipstvwnc	287

RESULT

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AAG17253

ID AAG17253 standard; Protein; 257 AA.

XX AAG17253;

AC AAG17253;

XX 17-OCT-2000 (first entry)

XX Arabidopsis thaliana protein fragment SEQ ID NO: 18203.

XX Arabidopsis thaliana.

OS Arabidopsis thaliana.

XX EP1033405-A2.

XX 06-SEP-2000.

XX 25-FEB-2000; 2000EP-0301439.

XX

Protein identification; signal transduction pathway; metabolic pathway;  
hybridisation assay; genetic mapping; gene expression control; promoter;  
termination sequence.

PR 25-FEB-1999; 99US-0121825.  
PR 05-MAR-1999; 99US-0123180.  
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PR	22-OCT-1999;	99US-0160989.	PR		28-APR-1999; 99US-0131449.
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PR	28-OCT-1999;	99US-0161992.	PR		11-MAY-1999; 99US-0134256.
PR	28-OCT-1999;	99US-0161993.	PR		14-MAY-1999; 99US-0134218.
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			PR		19-MAY-1999; 99US-0134941.
			PR		20-MAY-1999; 99US-0135124.
QY	68	MACVGGKDWTFYQORDRYATGRTNRATATGYWKGATGDKRTILRGKLVGMKRTLVFYQ 127	PR		21-MAY-1999; 99US-0135353.
Db	1	macvvgkdwfyqrdryatgtrnatatgywkgatgdkrtilrgkvlgmrtktilfyq 60	PR		24-MAY-1999; 99US-0135629.
			PR		25-MAY-1999; 99US-0136021.
			PR		27-MAY-1999; 99US-0136392.
QY	128	GRAPGRKTDVWHEFRLOQSHPPNHSLSPPKEDWVLCRVFKNTEGVICRDNMGSCFD 187	PR		28-MAY-1999; 99US-0136782.
Db	61	grapgrktdvwmhefrloqshppnhspspkedwvlcrrvfkntegvicrdmngscfd 120	PR		01-JUN-1999; 99US-0137222.
			PR		03-JUN-1999; 99US-0137528.
			PR		04-JUN-1999; 99US-0137502.
QY	188	ETASASLPPLMDPYINFDPSSYLSDDHYIINEHVPCFSNLSONOTLNSLTNSVSEL 247	PR		07-JUN-1999; 99US-0137724.
Db	121	etasaslpplmdpyinfdpssylsddhyiinehvpfcfsnlsqntlnsltnsvsel 180	PR		08-JUN-1999; 99US-0138094.
			PR		10-JUN-1999; 99US-0138540.
QY	248	KIPCKNPNLFTGGSASATLTGLDSFCSDDWVLRALLSOLTKTIDSLGPKESQSYGEGS 307	PR		14-JUN-1999; 99US-0139119.
Db	181	kipcnpnlftggsasatltgldsfcsddwvrlrallsoltktidslgpkesygyegs 240	PR		16-JUN-1999; 99US-0139452.
			PR		16-JUN-1999; 99US-0139453.
QY	308	SESLTIDIGIPSTVWNC 324	PR		17-JUN-1999; 99US-0139492.
Db	241	sesltidigipstvwnc 257	PR		18-JUN-1999; 99US-0139454.
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			PR		18-JUN-1999; 99US-0139459.
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			PR		18-JUN-1999; 99US-0139461.
			PR		18-JUN-1999; 99US-0139462.
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			PR		18-JUN-1999; 99US-0139763.
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			PR		24-JUN-1999; 99US-0140695.
			PR		28-JUN-1999; 99US-0140823.

RESULT 4

AAG22848  
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 DT 17-OCT-2000 (first entry)  
 XX  
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 25932.  
 XX  
 KW Protein identification; signal transduction pathway; metabolic pathway;  
 KW hybridisation assay; genetic mapping; gene expression control; promoter;  
 KW termination sequence.

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PR 08-JUL-1999; 99US-0142803.
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PR 25-OCT-1999; 99US-0161406.
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PR 26-OCT-1999; 99US-0161360.
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PR 28-OCT-1999; 99US-0161920.
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Db 1 macvvgkdwfyfysdrdkyatglrtnratatgywkatkdrtilrkgklygmrtklyfyq 60

QY 128 GRAPGRKTDWVHEFRLOGSHHPENHSLSPKEDWVLCRVFHKNTGVTICRDNMGSCFD 187
Db 61 grapgrktdwvhefrlogshhpnhalsspkedwvlcrvfhkntgvticrdnmgscfd 120

QY 188 ETASASLPPLMDPYINFDOEPSYSLSDDDHYIINHVPCFNLSONOTLNSLTNSVSEL 247
Db 121 etasaslpplmdpyinfdoepsyslssddhyiinehvpfcnlsonqlnslnlnsvsel 180

QY 248 KIPCKNPPLFTGGASATLTGLDSCSSDOMVLRLALSQTKIDGSLGPKESQSYGEGS 307
Db 181 kipcknpplftggasatlglscssdgmvlrallsqtkidgslgpkessygegs 240

QY 308 SESLLTDIGIPSTVWNC 324
Db 241 seslltdigipstvwnc 257

RESULT 5
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ID AAG17254 standard; Protein: 206 AA.
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AC AAG17254;  
XX 17-OCT-2000 (first entry)  
DT Arabidopsis thaliana protein fragment SEQ ID NO: 18204.  
XX  
DE  
XX  
KW Protein identification; signal transduction pathway; metabolic pathway;  
KW hybridisation assay; genetic mapping; gene expression control; promoter;  
KW termination sequence.  
XX  
OS Arabidopsis thaliana.  
XX  
PN EP1033405-A2.  
XX  
XX 06-SEP-2000.  
XX  
PF 25-FEB-2000; 2000EP-0301439.  
XX  
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PR 26-AUG-1999; 99US-0150884.
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PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
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PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
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PR 18-OCT-1999; 99US-0159584.
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PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
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PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
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PR 26-OCT-1999; 99US-0161361.
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PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 63.3%; Score 1112; DB 21; Length 206;
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Matches 206; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 179 RDNWGSCEFDETSASLPPLMDPIYINFDQEPSSYLSDDHHYIINEHVPCFSNLSONQTLS 238
Db 61 rdnwgscefdeataslpplmdpyinfdqepssylsddhyyiinehvpfcfsnlsqngtlns 120

QY 239 NLNTSVSELKIPCKNPFLTGGSASATLTGLDSDFCSDQWVLRALLSOLTKIDGSLGPK 298
Db 121 nlntsvselkipcknpfltggsasatltdgdsfcsdqwmvrlallsqitkldgslgpk 180

QY 299 ESQSYGEGSSSLLTDIGIPSTVWNC 324
Db 181 esqsygegsseslltdigipstvwnc 206
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## RESULT 6

AAG22849

ID AAG22849 standard; Protein; 206 AA.

XX AC AAG22849;

XX DT 17-OCT-2000 (first entry)

XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 25933.

XX KW Protein identification; signal transduction pathway; metabolic pathway;

XX KW hybridisation assay; genetic mapping; gene expression control; promoter;

XX OS Arabidopsis thaliana.

XX PN EP1033405-A2.

XX PD 06-SEP-2000.

XX PF 25-FEB-2000; 2000EP-0301439.

XX PR 25-FEB-1999; 99US-0121825.

XX PR 05-MAR-1999; 99US-0123180.

XX PR 09-MAR-1999; 99US-0123548.

XX PR 23-MAR-1999; 99US-0125788.

XX PR 25-MAR-1999; 99US-0126264.

XX PR 29-MAR-1999; 99US-0126785.

XX PR 01-APR-1999; 99US-0127462.

XX PR 06-APR-1999; 99US-0128234.

XX PR 08-APR-1999; 99US-0128714.

XX PR 16-APR-1999; 99US-0129845.

XX PR 19-APR-1999; 99US-0130077.

XX PR 21-APR-1999; 99US-0130449.

XX PR 23-APR-1999; 99US-0130510.

XX PR 23-APR-1999; 99US-0130891.

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XX PR 30-APR-1999; 99US-0132048.

XX PR 30-APR-1999; 99US-0132407.

XX PR 04-MAY-1999; 99US-0132484.

XX PR 05-MAY-1999; 99US-0132485.

XX PR 06-MAY-1999; 99US-0132486.

XX PR 06-MAY-1999; 99US-0132487.

XX PR 07-MAY-1999; 99US-0132863.

XX PR 11-MAY-1999; 99US-0134256.

XX PR 14-MAY-1999; 99US-0134218.

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XX PR 18-MAY-1999; 99US-0134768.

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XX PR 08-JUN-1999; 99US-0138094.

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XX PR 16-JUN-1999; 99US-0139452.

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KW hybridisation assay; genetic mapping; gene expression control; promoter;  
KW termination sequence.  
XX OS Arabidopsis thaliana.  
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XX PD 06-SEP-2000.  
XX PF 25-FEB-2000; 2000EP-0301439.  
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DT 18-OCT-2000 (first entry)
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KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
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AC AAG17255;  
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DT 17-OCT-2000 (first entry)  
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KW Protein identification; signal transduction pathway; metabolic pathway;  
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Query Match 56.7%; Score 997; DB 21; Length 185;  
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XX KW Protein identification; signal transduction pathway; metabolic pathway;  
XX KW hybridisation assay; genetic mapping; gene expression control; promoter;  
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XX OS Arabidopsis thaliana.  
XX PN EP1033405-A2.  
XX PD 06-SEP-2000.  
XX PF 25-FEB-2000; 2000EP-0301439.  
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Query Match 56.7%; Score 997; DB 21; Length 185;
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DT 18-OCT-2000 (first entry)
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DE Arabidopsis thaliana protein fragment SEQ ID NO: 57542.
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KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
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OS Arabidopsis thaliana.
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PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
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QY 242 NSVSELKIPCKNPPLFTGSGASATLTGLDSCSSQMVLRALLSQTLDKIDSLGPKESQ 301
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XX AC AAG45827;
XX DT 18-OCT-2000 (first entry)
XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 57582.
XX KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX OS Arabidopsis thaliana.
XX PN EP1033405-A2.
XX PD 06-SEP-2000.
XX PF 25-FEB-2000; 2000EP-0301439.
XX PR 25-FEB-1999; 99US-0121825.
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PR 23-MAR-1999; 99US-0125788.
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PR 99US-0132485.

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Query Match 42.9%; Score 754; DB 21; Length 143;

Best Local Similarity 100.0%; Pred. No. 2.4e-69;

Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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AAG06726  
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XX AAG06726;

XX 17-OCT-2000 (first entry)

XX Arabidopsis thaliana protein fragment SEQ ID NO: 3605.

XX Protein identification; signal transduction pathway; metabolic pathway;  
XX hybridisation assay; genetic mapping; gene expression control; promoter;  
XX termination sequence.

XX Arabidopsis thaliana.

XX EP1033405-A2.

XX 06-SEP-2000.

XX 25-FEB-2000; 2000EP-0301439.

XX 25-FEB-1999; 99US-0121825.

XX 05-MAR-1999; 99US-0123180.

XX 23-MAR-1999; 99US-0123548.

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XX 01-APR-1999; 99US-0126785.

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Query Match 31.7%; Score 557; DB 21; Length 329;
Best Local Similarity 42.2%; Pred. No. 1.5e-48;
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QY 285 L 285
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AC AAG46660;
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XX 18-OCT-2000 (first entry)
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KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
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PD 06-SEP-2000.
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XX 25-FEB-2000; 2000EP-0301439.
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XX 25-FEB-1999; 99US-0121825.
XX 05-MAR-1999; 99US-0123180.
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PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.

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PR	20-JUL-1999;	99US-0144352.
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PR	21-JUL-1999;	99US-0145086.
PR	21-JUL-1999;	99US-0145088.
PR	21-JUL-1999;	99US-0145085.
PR	22-JUL-1999;	99US-0145087.
PR	22-JUL-1999;	99US-0145089.
PR	22-JUL-1999;	99US-0145192.
PR	23-JUL-1999;	99US-0145145.
PR	23-JUL-1999;	99US-0145218.
PR	23-JUL-1999;	99US-0145224.
PR	26-JUL-1999;	99US-0145276.
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PR	27-JUL-1999;	99US-0145919.
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PR	02-AUG-1999;	99US-0146386.
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PR	10-AUG-1999;	99US-0148171.
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PR	13-AUG-1999;	99US-0148684.
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PR	27-AUG-1999;	99US-0151080.
PR	30-AUG-1999;	99US-0151303.
PR	31-AUG-1999;	99US-0151438.
PR	01-SEP-1999;	99US-0151930.
PR	07-SEP-1999;	99US-0152363.
PR	10-SEP-1999;	99US-0153070.
PR	13-SEP-1999;	99US-0153758.
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PR	12-OCT-1999;	99US-0158369.
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PR	14-OCT-1999;	99US-0159637.
PR	14-OCT-1999;	99US-0159638.
PR	18-OCT-1999;	99US-0159584.
PR	21-OCT-1999;	99US-0160741.
PR	21-OCT-1999;	99US-0160767.
PR	21-OCT-1999;	99US-0160768.
PR	21-OCT-1999;	99US-0160770.
PR	21-OCT-1999;	99US-0160814.
PR	21-OCT-1999;	99US-0160815.
PR	22-OCT-1999;	99US-0160880.
PR	22-OCT-1999;	99US-0160981.
PR	22-OCT-1999;	99US-0160989.
PR	25-OCT-1999;	99US-0161404.
PR	25-OCT-1999;	99US-0161405.
PR	25-OCT-1999;	99US-0161406.
PR	26-OCT-1999;	99US-0161359.
PR	26-OCT-1999;	99US-0161360.
PR	26-OCT-1999;	99US-0161361.
PR	28-OCT-1999;	99US-0161920.
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PR	29-OCT-1999;	99US-0162142.

Query Match 31.7%; Score 557; DB 21; Length 329;

Best Local Similarity 42.2%; Pred. No. 1.5e-48;

Matches 127; Conservative 42; Mismatches 78; Indels 54; Gaps 11;

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QY 62 PWDIPKMACVGGKDWYFYQSQRDKYATGLRTNRATATGYKATGKDRITLKKGLVGMRK 121

Db 59 pwelpykakigekekwyfcvdrkyptglrtnrataqgywkatgkdkkeifrgkslvgmkk 118

QY 122 TLVfyQGRAPGRKTDWVHFERLOG---SHPPNHSLSSPKEDWVLCRVPHKNTGEG--- 175

Db 119 tlvyfyrgrapqgktnwvwmheyridgklsahnp-----ktaknewvrcrvfhktaggkki 174

QY 176 -VICRDNMGSCFDEITASASLPPLMD--PYINFDPQPSYLSDDHHYIINEHVPCFSNLSQ 232

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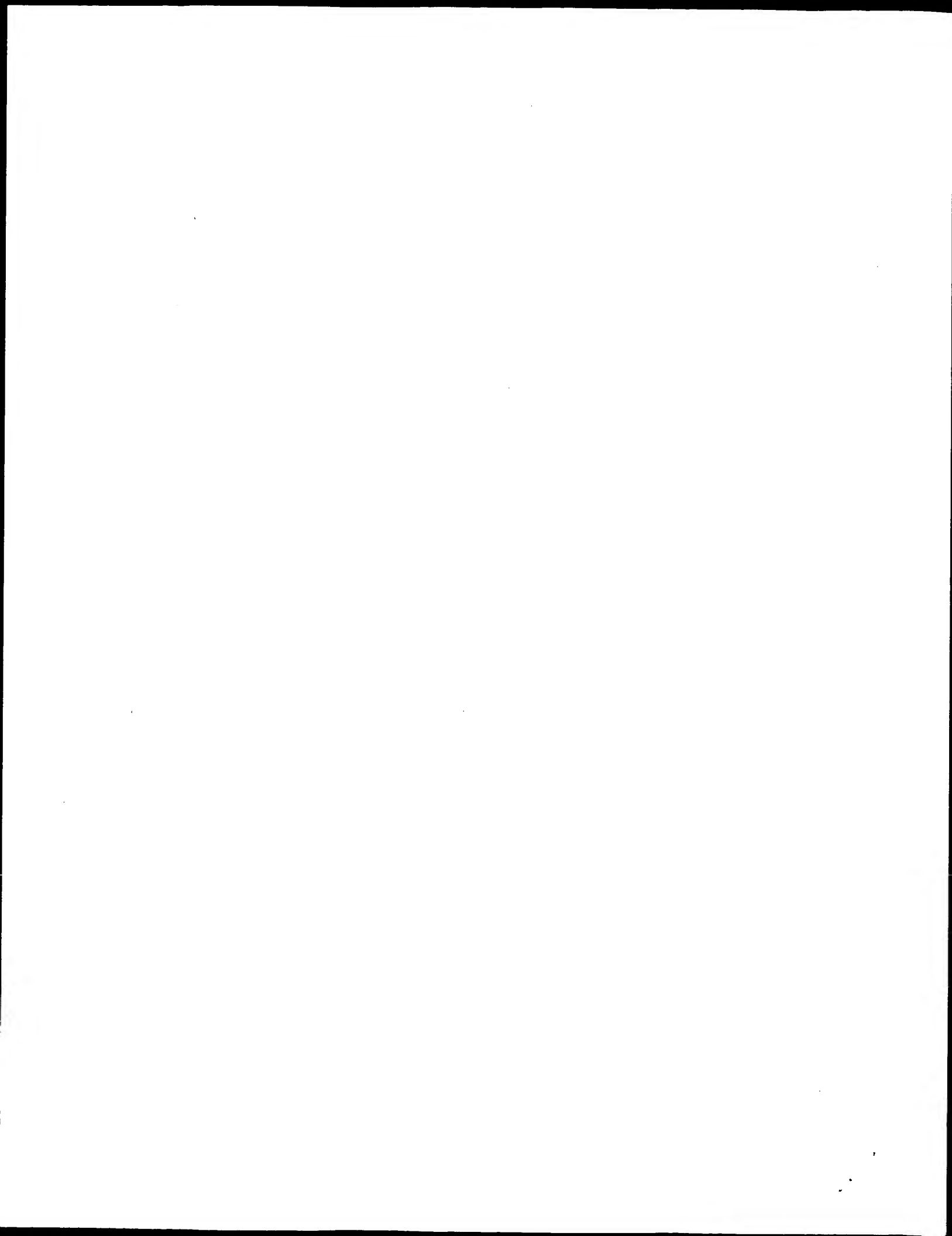
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Db 273 m 273

Search completed: July 15, 2002, 06:56:42

Job time: 229 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 15, 2002, 06:54:48 ; Search time 13.14 Seconds  
(without alignments)  
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Title: US-09-889-926-2  
Perfect score: 1757  
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Scoring table: BLOSUM62  
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Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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2	106	6.0	1872	1 US-08-646-715-14	Sequence 14, Appl
3	106	6.0	1893	1 US-08-188-582-11	Sequence 11, Appl
4	106	6.0	1893	1 US-08-646-715-11	Sequence 11, Appl
5	95	5.4	2938	5 PCT-US94-00198-3	Sequence 3, Appl
6	95	5.4	3969	4 US-08-061-376-5	Sequence 5, Appl
7	94	5.4	623	4 US-09-104-068-4	Sequence 4, Appl
8	94	5.4	637	4 US-09-104-068-2	Sequence 2, Appl
9	87.5	5.0	1704	4 US-08-485-355B-40	Sequence 40, Appl
10	84.5	4.8	1182	4 US-09-287-354-6	Sequence 6, Appl
11	81.5	4.6	504	4 US-07-932-915-2	Sequence 2, Appl
12	81.5	4.6	504	5 PCT-US91-05826-2	Sequence 2, Appl
13	81.5	4.6	1207	4 US-09-287-354-5	Sequence 5, Appl
14	81.5	4.6	1481	4 US-09-251-645-14	Sequence 14, Appl
15	80.5	4.6	1863	2 US-08-603-753D-2	Sequence 2, Appl
16	80.5	4.6	1863	4 US-09-099-753-2	Sequence 2, Appl
17	80.5	4.6	1863	4 US-08-986-106-2	Sequence 2, Appl
18	80.5	4.6	1863	4 US-09-007-678B-49	Sequence 49, Appl
19	80	4.6	1142	2 US-08-993-118-7	Sequence 7, Appl
20	80	4.6	1142	3 US-08-845-528C-7	Sequence 7, Appl
21	80	4.6	1142	4 US-09-061-709-2	Sequence 2, Appl
22	79	4.5	427	4 US-08-506-296B-56	Sequence 56, Appl
23	79	4.5	665	4 US-08-506-296B-68	Sequence 68, Appl
24	79	4.5	1253	4 US-08-506-296B-14	Sequence 14, Appl
25	79	4.5	2183	3 US-08-746-111-5	Sequence 5, Appl
26	79	4.5	3898	4 US-08-750-717-2	Sequence 2, Appl
27	79	4.5	4654	4 US-08-476-515A-84	Sequence 84, Appl

ALIGNMENTS

RESULT 1  
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; Sequence 14; Application US/08188582  
; Patent No. 5534410  
; GENERAL INFORMATION:  
; APPLICANT: Tjian, Robert  
; APPLICANT: Comai, Lucio  
; APPLICANT: Dynlacht, Brian D.  
; APPLICANT: Hoey, Timothy  
; APPLICANT: Ruppert, Siegfried  
; APPLICANT: Tanese, Naoko  
; APPLICANT: Wang, Edith  
; APPLICANT: Weinzierl, Robert O.J.  
; TITLE OF INVENTION: TATA-BINDING PROTEIN ASSOCIATED FACTORS,  
; NUCLEIC ACIDS ENCODING TAFS AND METHODS OF USE  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT  
; STREET: 4 Embarcadero Center, Suite 3400  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-4187  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/188,582  
; FILING DATE: 28-JAN-1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Osman, Richard A  
; REGISTRATION NUMBER: 36, 627  
; REFERENCE/DOCKET NUMBER: A-57650-2/AJT/RAO  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 781-1989  
; TELEFAX: (415) 398-3249  
; TELEX: 910 277299  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1872 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-188-582-14

28	79	4.5	4655	4	US-08-652-877-84	Sequence 84, Appl
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30	79	4.5	4655	4	US-08-652-877-88	Sequence 88, Appl
31	79	4.5	4655	4	US-08-652-877-90	Sequence 90, Appl
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33	78	4.4	837	3	US-09-012-710-12	Sequence 12, Appl
34	78	4.4	837	4	US-09-556-273-12	Sequence 12, Appl
35	77.5	4.4	765	1	US-08-425-061-19	Sequence 19, Appl
36	77.5	4.4	765	2	US-08-825-886-19	Sequence 19, Appl
37	77.5	4.4	900	1	US-08-425-061-20	Sequence 20, Appl
38	77.5	4.4	900	2	US-08-825-886-20	Sequence 20, Appl
39	77.5	4.4	914	1	US-08-425-061-21	Sequence 21, Appl
40	77.5	4.4	914	2	US-08-825-886-21	Sequence 21, Appl
41	77.5	4.4	1202	1	US-08-425-061-22	Sequence 22, Appl
42	77.5	4.4	1202	2	US-08-825-886-22	Sequence 22, Appl
43	77.5	4.4	1363	1	US-08-425-061-23	Sequence 23, Appl
44	77.5	4.4	1363	2	US-08-825-886-23	Sequence 23, Appl
45	77.5	4.4	1852	1	US-08-425-061-24	Sequence 24, Appl

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Query Match      6.08; Score 106; D3 1; Length 1872;
Best Local Similarity 19.9%; Pred. No. 0.037;
Matches 79; Conservative 51; Mismatches 125; Indels 142; Gaps 21;

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QY      212  LSDQ-----HHYIINEHVCPFSLSQN-----QTLSNLT----- 241
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QY      285  LSQLTKTID----GSLGPKESQSYGEGSSLLTDIGI 317
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RESULT      2
US-08-646-715-14
: Sequence 14, Application US/08646715
: Patent No. 5637686
: GENERAL INFORMATION:
: APPLICANT: Tjian, Robert
: APPLICANT: Comai, Lucio
: APPLICANT: Dynlacht, Brian D.
: APPLICANT: Hoey, Timothy
: APPLICANT: Rupprecht, Siegfried
: APPLICANT: Tanese, Naoko
: APPLICANT: Wang, Edith
: APPLICANT: Weinzierl, Robert O.J.
: TITLE OF INVENTION: TATA-BINDING PROTEIN ASSOCIATED FACTORS,
: NUCLEIC ACIDS ENCODING TAFs AND METHODS OF USE
: NUMBER OF SEQUENCES: 36
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: FLEHR, ROBBACH, TEST, ALBRITTON & HERBERT
: STREET: 4 Embarcadero Center, Suite 3400
: CITY: San Francisco
: STATE: California
: COUNTRY: USA
: Zip: 94111-4187
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/646,715
: FILING DATE: 09-MAY-1996
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/188,582
: FILING DATE: 28-JAN-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Osman, Richard A.
: REGISTRATION NUMBER: 36,627
: REFERENCE/DOCKET NUMBER: A-57650-2/AJT/RAO
: TELECOMMUNICATION INFORMATION:

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; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1872 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-646-715-14

Query Match          6.0%; Score 106; DB 1; Length 1872;
Best Local Similarity 19.9%; Pred. No. 0.057;
Matches 79; Conservative 51; Mismatches 125; Indels 142; Gaps 21;

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   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1383 VTLSIIESTINMRDLDPNTYFHTPNVAKV-KDYTKIITRPMDLOT-LREN----- 1433
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 101 WKATGKDRITLRKGLVGRKRTLVFYOGRAPRGKRTDWMVHEFR-----LQGSHPH 152
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1434 -----VRKRL--YPSR-----EERHEHLIVKNSATYNGP 1462
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QY 153 NHISSPKEDWV-LCRYFHKNTGVLICRDNMGSCFDETAASLPPLMDPYINFDOEPSSY 211
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1463 KHSLTQISQSMDLCDKLEKEKDKLAR-----LEKANPLLD---DDQVAFSF 1509
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 212 LSDD-----HHYIINEHVPCFNSLQN-----QTINSLNT----- 241
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
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QY 242 ---NSVSELKIPCKNPPLFTGGSAS-----ATLGLD-----SFGSSDQMVLRAL 284
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QY 285 LSQITKID-----GSLGPKESQSYGEGSSSLLTDIGI 317
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RESULT 3
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; Sequence 11, Application US/08188582
; Patent No. 5534410
;
; GENERAL INFORMATION:
;
; APPLICANT: Tjian, Robert
; APPLICANT: Comai, Lucio
; APPLICANT: Dynlacht, Brian D.
; APPLICANT: Hoey, Timothy
; APPLICANT: Ruppert, Siegfried
; APPLICANT: Tanese, Naoko
; APPLICANT: Wang, Edith
; APPLICANT: Weinzierl, Robert O.J.
;
; TITLE OF INVENTION: TATA-BINDING PROTEIN ASSOCIATED FACTORS,
;
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING TAFs AND METHODS OF USE
;
; NUMBER OF SEQUENCES: 36
;
; CORRESPONDENCE ADDRESS:
;
; ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
;
; ZIP: 94111-4187
;
; COMPUTER READABLE FORM:
;
; MEDIUM TYPE: Floppy disk
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; COMPUTER: IBM PC compatible
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; OPERATING SYSTEM: PC-DOS/MS-DOS

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SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/188,582  
FILING DATE: 28-JAN-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Osman, Richard A  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: A-57650-2/AJT/RAO  
TELEPHONE: (415) 781-1989  
TELEFAX: (415) 398-3249  
TELECOMMUNICATION INFORMATION:  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1893 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-188-582-11

Query Match 6.0%; Score 106; DB 1; Length 1893;  
Best Local Similarity 19.9%; Pred. No. 0.058;  
Matches 79; Conservative 51; Mismatches 125; Indels 142; Gaps 21;

QY 1 METEEMKSS--ISMVEAKLPP-----GFRFHPKDELVCYLMR--RSLNNHRRPPL 50  
Db 1351 IESADEVRKSLVLFKPKQQLPPKKRRVGTTH-----CDYLNRPKHSIHRRTDPM 1403  
QY 51 VLIQV-----DLNKEPMDIPKMACVGGKDWYFYQSQRDKYATGLRTNATATGY 100  
Db 1404 VTLSSILESIINDRDLPTNTPFHTPVNAKV-VKDYKIIITRPMDLQT-LREN----- 1454  
QY 101 WKATGKDRITLRKGLVGMKRTLVFYQGRAPGRKTDWMHEFR-----LQSHHPP 152  
Db 1455 -----VRKRL--YPSR-----EPRHLELIVKNSATYNGP 1483  
QY 153 NLSLSPKEDWV-LCRVFHKTGVCICRDNMGSCFDETSASLPLMDPYINFDQPSY 211  
Db 1484 KHSLTQISQMLDLCDEKLEKEDKLAR-----LEKAINPLLD---DDQVAFSF 1530  
QY 212 LSDD-----HHYIINEHVPCFNLSON-----QTLNSNLT----- 241  
Db 1531 ILDNIVTKMMAVPDSWPFHPVKNKFPDYKVIYNPMDLETIRKNSIKHKYQSRESFL 1590  
QY 242 ---NSVSELKIPCKNPNPLTGGAS-----ATLTGLD-----SFCSSDQVLRAL 284  
Db 1591 DDVNLILANSVKYNGPESQYTKTAQEIIVNVCYQTLTEYDEHLTQLEKDICTAKEAALAE- 1649  
QY 285 LSQTKID---GSLGPKESQSYGEGSSSLLTDIGI 317  
Db 1650 -AELESIDPMTGPTTPQPPDLYDTNTSLMSRDSAV 1685

## RESULT 4

US-08-646-715-11  
Sequence 11, Application US/08646715  
Patent No. 5637686

## GENERAL INFORMATION:

APPLICANT: Tjian, Robert  
APPLICANT: Comai, Lucio  
APPLICANT: Dynlacht, Brian D.  
APPLICANT: Hoey, Timothy  
APPLICANT: Ruppert, Siegfried  
APPLICANT: Tanese, Naoko  
APPLICANT: Wang, Edith  
APPLICANT: Weinzierl, Robert O.J.  
TITLE OF INVENTION: TATA-BINDING PROTEIN ASSOCIATED FACTORS,  
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING TAFS AND METHODS OF USE  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT

STREET: 4 Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-4187  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/646,715  
FILING DATE: 09-MAY-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/188,582  
FILING DATE: 28-JAN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Osman, Richard A  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: A-57650-2/AJT/RAO  
TELEPHONE: (415) 781-1989  
TELEFAX: (415) 398-3249  
TELECOMMUNICATION INFORMATION:  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1893 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-646-715-11

Query Match 6.0%; Score 106; DB 1; Length 1893;  
Best Local Similarity 19.9%; Pred. No. 0.058;  
Matches 79; Conservative 51; Mismatches 125; Indels 142; Gaps 21;

QY 1 METEEMKSS--ISMVEAKLPP-----GFRFHPKDELVCYLMR--RSLNNHRRPPL 50  
Db 1351 IESADEVRKSLVLFKPKQQLPPKKRRVGTTH-----CDYLNRPKHSIHRRTDPM 1403  
QY 51 VLIQV-----DLNKEPMDIPKMACVGGKDWYFYQSQRDKYATGLRTNATATGY 100  
Db 1404 VTLSSILESIINDRDLPTNTPFHTPVNAKV-VKDYKIIITRPMDLQT-LREN----- 1454  
QY 101 WKATGKDRITLRKGLVGMKRTLVFYQGRAPGRKTDWMHEFR-----LQSHHPP 152  
Db 1455 -----VRKRL--YPSR-----EPRHLELIVKNSATYNGP 1483  
QY 153 NLSLSPKEDWV-LCRVFHKTGVCICRDNMGSCFDETSASLPLMDPYINFDQPSY 211  
Db 1484 KHSLTQISQMLDLCDEKLEKEDKLAR-----LEKAINPLLD---DDQVAFSF 1530  
QY 212 LSDD-----HHYIINEHVPCFNLSON-----QTLNSNLT----- 241  
Db 1531 ILDNIVTKMMAVPDSWPFHPVKNKFPDYKVIYNPMDLETIRKNSIKHKYQSRESFL 1590  
QY 242 ---NSVSELKIPCKNPNPLTGGAS-----ATLTGLD-----SFCSSDQVLRAL 284  
Db 1591 DDVNLILANSVKYNGPESQYTKTAQEIIVNVCYQTLTEYDEHLTQLEKDICTAKEAALAE- 1649  
QY 285 LSQTKID---GSLGPKESQSYGEGSSSLLTDIGI 317  
Db 1650 -AELESIDPMTGPTTPQPPDLYDTNTSLMSRDSAV 1685

## RESULT 5

PCT-US94-00198-3  
Sequence 3, Application PC/TUS9400198  
GENERAL INFORMATION:  
APPLICANT: Schering Corp.  
TITLE OF INVENTION: RAS Associated GAP Proteins

```

: NUMBER OF SEQUENCES: 6
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Schering Corp.
: STREET: 1 Girald Farms
: CITY: Madison
: STATE: New Jersey
: COUNTRY: USA
: ZIP: 94304-1104
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: Macintosh
: OPERATING SYSTEM: 6.0.8
: SOFTWARE: Microsoft Word 5.1a
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US94/00198
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/004,824
: FILING DATE: 15-JAN-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: Lunn, Paul G.
: REGISTRATION NUMBER: 32,743
: REFERENCE/DOCKET NUMBER: DX0352 PCT
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (201)822-7255
: TELEFAX: (201)822-7039
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2938 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: ORIGINAL SOURCE:
: ORGANISM: Saccharomyces cerevisiae
: PCT-US94-00198-3

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Query Match      5.4%; Score 95; DB 5; Length 2938;
Best Local Similarity 21.7%; Pred. No. 1.6;
Matches 69; Conservative 46; Mismatches 121; Indels 82; Gaps 15;

QY   31 ELVCVYLRRSLHNRPLVLIOVDLNKCEPWDI-----PKMACVGCGKWDFYS 80
Db   58 DLTIDYIQRTISASNH-----VEPTCKVKTKVAPLLISHSTELGVNHNLDFOCE 109

QY   81 QDRKYATGLRTRNATATGYWKATGKDRTLIRGKLGVGRMKTILVFYOGRAPGRKTDW- 139
Db   110 YLTDKNLLAYLDLOHLSSYMK----RTFHSLLYLYAKAFLEFWIMARPK---EYVK 160

QY   140 MHIEFRIQSGHHPPNHSLSRPEDWLCRVFKHKNTGEVICRDNNGS-CFDETASALPLPM 198
Db   161 IYNNLITSSDYPSSS-----SDNGSNNSDKTISQLVSILL 197

QY   199 --DPVINTEQPSSVL---SDDHVIINEHVHPCFSNLSONQTLSNLTNSVELAIPCK - 252
Db   198 FDDVYSTF--SGSSLTLTNWNNDHHYHLHH-----SSSSSKTTINTSPNSIKTSKIOWS 249

QY   253 -----NPNFLFTGGASAT--LTGDDSCSDQMWLRALLSQTKIDGSLGPRESQSY 303
Db   250 VNAGSNVSPQSFGTGNDASPTSPNASLSSPLTN--ILGYPLSPITSLTIGQANTSTSI-- 305

QY   304 GEGSSSESLTDIGIPSTV 321
Db   306 ---TAATTKTADTPSTM 320
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RESULT: 6  
US-08-061-376-5  
; Sequence 5, Application US/08061376  
; Patent No. 6175000  
; GENERAL INFORMATION:

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1  APPLICANT: Evans, Glen A.
2  APPLICANT: Djabali, Matek
3  APPLICANT: Selleri, Lucia
4  APPLICANT: Parry, Pauline
5  TITLE OF INVENTION: CHARACTERIZATION OF A CHROMOSOMAL
6  TITLE OF INVENTION: TRANSLOCATION BREAKPOINT ASSOCIATION
7  NUMBER OF SEQUENCES: 12
8  CORRESPONDENCE ADDRESS:
9  ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
10 STREET: 444 South Flower Street, Suite 2000
11 CITY: Los Angeles
12 STATE: California
13 COUNTRY: USA
14 ZIP: 90071
15 COMPUTER READABLE FORM:
16 MEDIUM TYPE: Floppy disk
17 COMPUTER: IBM PC compatible
18 OPERATING SYSTEM: PC-DOS/MS-DOS
19 SOFTWARE: PatentIn Release #1.0, Version #1.25
20 CURRENT APPLICATION DATA:
21 APPLICATION NUMBER: US-08/061,376
22 FILING DATE: 13-MAY-1993
23 CLASSIFICATION: 435
24 ATTORNEY/AGENT INFORMATION:
25 NAME: Reiter, Stephen E.
26 REGISTRATION NUMBER: 31,192
27 REFERENCE/DOCKET NUMBER: P41 9387
28 TELECOMMUNICATION INFORMATION:
29 TELEPHONE: (619)546-4737
30 TELEFAX: (619)546-9392
31 INFORMATION FOR SEQ ID NO: 5:
32 SEQUENCE CHARACTERISTICS:
33 LENGTH: 3969 amino acids
34 TYPE: amino acid
35 STRANDEDNESS: unknown
36 TOPOLOGY: unknown
37 MOLECULE TYPE: protein
38 US-08-061-376-5

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[illegible]

RESULT 7  
US-09-104-068-4  
; Sequence 4, Application US/09104068  
; Patent No. 623882







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Qv 111 1RKGKLVGMKKTIVFYOGAPRG--RKTDWMHEFRQGS-----HP----- 151

Db 87 LPPGFLQGPDKDPLSVVEGGRNGERKANWLGSGEGLRWKEAMLAHPLAFQCPACPPRYG 146  
QY 152 ---PNHSLSSPKEDWVLCRVFKHKTGVCICRDNMGSCFDETSASASLPLMDPYINFDQEP 208  
Db 147 PLIPEHSSGHPKSDPAFRPLH-----CPLETKILERAPWVPTCLPPYL----- 193  
QY 209 SSYLSDDHHYIINEHVPCFNSLSONQTLNSLTVSVSELKIPCKNPMPNPLFTGGG-----AS 264  
Db 194 -----MSSLPPERSYDWPLA-----PSPWVYSGSQPKVPS 223  
QY 265 ATLTLGLDSECSDDQWVLRALLSQLTKIDGSL-----GPKESQSYGE--- 305  
Db 224 AFSGSKGFYHKDPNLRPAKEPLAASESGMLGLAPGSHLQQAACDAEGPSLHQDGETGA 283  
QY 306 GSSESLL-TDIGIPSTV 321  
Db 284 GRQCNLCVPFLGYPDV 300

## RESULT 14

US-09-251-645-14  
; Sequence 14, Application US/09251645  
; Patent No. 6281413

## GENERAL INFORMATION:

; APPLICANT: Kramer, Vance C.  
; APPLICANT: Morgan, Michael K.  
; APPLICANT: Anderson, Arne R.  
; APPLICANT: Hart, Hope  
; APPLICANT: Warren, Gregory W.  
; APPLICANT: Dunn, Martha  
; APPLICANT: Chen, Jeng S.

; TITLE OF INVENTION: NOVEL INSECTICIDAL TOXINS FROM PHOTORHABDUS LUMINESCENS  
; FILE REFERENCE: CGC1963/A  
; CURRENT APPLICATION NUMBER: US/09/251,645  
; CURRENT FILING DATE: 1999-02-17

; NUMBER OF SEQ ID NOS: 22

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 14

; LENGTH: 1481

; TYPE: PRT

; ORGANISM: Photorhabdus luminescens

US-09-251-645-14

Query Match 4.6%; Score 81.5; DB 4; Length 1481;

Best Local Similarity 22.5%; Pred. No. 16;

Matches 78; Conservative 33; Mismatches 90; Indels 145; Gaps 23;

QY 74 KDWYFSQRDRKYATGL-RTNRTATGYWKA-----TG--KDRTLRKGLVGMKRT--- 122  
Db 814 KNW-----YATGIPEVDNLSAGYWRGDTQAFGTPTHTLWKEGKDVPLTPEDDH 864  
QY 123 LVFYQGRAPRG-----RKTDWMHFRQCSHPPNHSLSPPKEDW---V 164  
Db 865 NLYWLNKALGQPLRSELXGLDGSQAQKIPYIVTESRPQVROLQDNTILSPVL--WASV 922  
QY 165 LCRVFHK-----NTEGVCIRDNMGSCFDETSASILP-----PLMDPYINFDQEP--- 208  
Db 923 ERSYHYERIISDPQCNQDITLSSDLFGQPLKQ-VSVQYPRNKKTNPYP--DTLPDTL 979  
QY 209 --SSYLSDD-----HVVINE-----HVP----- 225  
Db 980 FASSY--DQOQQLRLTYOQSWHHLIANELRVGLPDCGTRSDAFTYDAKHVPVDGLNLE 1037  
QY 226 --CFSN-----LSQNTLNSLTVSVSELKIPCKNPMPNPLFTGGASATLTGLDS 272  
Db 1038 ALCAENSLIADDKPREYLNQRTF-----YTDGKTDKNETPLKT-----PTQALIA 1085  
QY 273 ECSSDQWVLRALLSQ--LTKIDGSLGPKESQSYGEGSSSELTLTDIG 316  
Db 1086 FTET-----AVLTSSLASFDDGGITPDE-----LPGLLTQAG 1117

## RESULT 15

US-08-603-753D-2

; Sequence 2, Application US/08603753D

; Patent No. 5891857

## GENERAL INFORMATION:

; APPLICANT: HOLT, JEFFREY T.  
; APPLICANT: JENSEN, ROY A.  
; APPLICANT: PAGE, DAVID L.  
; APPLICANT: KING, MARY-CLAIRE  
; APPLICANT: SZABO, CSILLA I.  
; APPLICANT: JETTON, THOMAS L.  
; APPLICANT: ROBINSON-BENION, CHERYL L.  
; APPLICANT: THOMPSON, MARILYN E.

; TITLE OF INVENTION: CHARACTERIZED BRCA1 AND BRCA2

; TITLE OF INVENTION: PROTEINS AND SCREENING AND THERAPEUTIC METHODS BASED ON  
; TITLE OF INVENTION: CHARACTERIZED BRCA1 AND BRCA2 PROTEINS.

; NUMBER OF SEQUENCES: 29

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: ARLES A. TAYLOR, JR.

; STREET: SUITE 1401, UNIVERSITY TOWER, 3100 TOWER

; CITY: DURHAM

; STATE: NORTH CAROLINA

; COUNTRY: USA

; ZIP: 27707

## COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.50 inch, 800 kb storage

; COMPUTER: IBM PC/XT/AT compatible

; OPERATING SYSTEM: Windows 3.1

; SOFTWARE: WORD PERFECT 6.1 and ASCII

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/603,753D

; FILING DATE: 20 FEB 1996

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: U.S. 08/373,799

; FILING DATE: 17 JAN 1995

; ATTORNEY/AGENT INFORMATION:

; NAME: ARLES A. TAYLOR, JR.

; REGISTRATION NUMBER: 39,395

; REFERENCE/DOCKET NUMBER: 1242/2

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (919) 493-8000

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; TELEX:

; INFORMATION FOR SEQ ID NO: 2:

## SEQUENCE CHARACTERISTICS:

; LENGTH: 1863

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: unknown

; MOLECULE TYPE: protein

; HYPOTHETICAL: no

; ANTI-SENSE: no

; ORIGINAL SOURCE:

; ORGANISM: Homo sapiens

; INDIVIDUAL ISOLATE:

; DEVELOPMENTAL STAGE: adult

; TISSUE TYPE: female breast

; CELL TYPE: ductal carcinoma in situ, invasive

; CELL LINE: breast cancer and normal breast tissue

; ORGANELLES: not derived from a cell line

; IMMEDIATE SOURCE:

; LIBRARY: cDNA library derived from human

; CLONE: obtained using published sequence

; POSITION IN GENOME:

; CHROMOSOME/SEGMENT: unknown

; MAP POSITION: unknown

; UNITS: unknown

; FEATURE:

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; NAME/KEY:  BRCA1 protein
; LOCATION:  1 to 1863
; IDENTIFICATION METHOD:  observation of mRNA and
; IDENTIFICATION METHOD:  antisense inhibition of BRCA1 gene
; OTHER INFORMATION:  BRCA1 protein has a negative
; OTHER INFORMATION:  regulatory effect on growth of human mammary cells.
; PUBLICATION INFORMATION:
; AUTHORS:  Miki, Y., et. al.
; TITLE:  A strong candidate gene for the breast and
; TITLE:  ovarian cancer susceptibility gene BRCA1.
; JOURNAL:  Science
; VOLUME:  266
; PAGES:  66-71
; DATE:  1994
; RELEVANT RESIDUES IN SEQ ID NO:  2:  granin box
; RELEVANT RESIDUES IN SEQ ID NO:  domain at amino acids 1214-1223
US-08-603-753D-2

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Query Match	4.6%	Score	80.5	DB	2	Length	1863
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QY	53	IQVDLNNK---CE--PWDIPKMACVGGKDWFFYSQRDKYATGLRNRA-TATGYW----	101				
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QY	338	KKVDLNADPLCERKEWNKQLPC-----SENPRDTEVPWITLNSSIQKNEWFSRSD	390				
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QY	102	-----KATGKDTILRKGLVMKTLVfyOGRApRGRKTDWY---HEERLOGSHHP	151				
DB							
QY	391	ELGSDDDSHDGESESNKAVADVLDVLNEVDYSGSS---EKIDLLASOPHEALICKSDRV	447				
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QY	152	PNHSLSSPKEDWLCRVFHKH-----TEGVICRDNMGSCFDEtASASLPPLMDPYI	202				
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QY	309	ESL	311				
DB							
QY	618	RHI	620				
DB							

Search completed: July 15, 2002, 06:57:04  
Job time: 136 sec

